

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:43:13 ; Search time 21 Seconds
(without alignments)
3105.612 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502
Sequence: 1 MRTVLTMKASVEMFLVLL.....QYVPRIIQICTEPNSQPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	15.8	3124	2 A40020	collagen alpha 1(X
2	504.5	14.4	3137	2 A37797	collagen alpha 3(V
3	501.5	14.3	496	2 A37979	cartilage matrix p
4	490	14.0	493	2 A33809	cartilage matrix p
5	490	14.0	500	2 S66522	cartilage matrix p
6	471.5	13.5	3176	2 CGHU3A	collagen alpha 3(V
7	331	9.5	1857	2 S31212	collagen alpha 1(X
8	331	9.5	1888	2 S78476	collagen alpha 1(X
9	329.5	9.4	2944	2 A54849	collagen alpha 1(V
10	329	9.4	1747	2 A45974	collagen alpha 1(X
11	314.5	9.0	567	2 T28767	hypothetical prote
12	298	8.5	741	2 T46488	hypothetical prote
13	280.5	8.0	929	2 T51037	type XII collagen
14	279	8.0	3051	2 S42373	hypothetical prote
15	266	7.6	2813	1 VWHU	von Willebrand fac
16	262.5	7.5	843	2 A40970	undulin 1 - human
17	252.5	7.2	1019	1 A32856	collagen alpha 1(V
18	231	6.6	1153	1 RWHU1B	cell surface glyco
19	229	6.5	550	2 T23760	hypothetical prote
20	229	6.5	1153	2 S00551	leukocyte surface
21	228	6.5	1163	1 RWHU1C	cell surface glyco
22	226.5	6.5	427	2 G00039	von Willebrand fac
23	226.5	6.5	1025	2 S34839	collagen alpha 1(V
24	213.5	6.1	414	2 P50323	von Willebrand fac
25	213.5	6.1	1286	2 A88396	protein M01B10.2 [
26	210.5	6.0	2098	2 T18397	protein CTRP - mal
27	209.5	6.0	1022	2 S04111	collagen alpha 2(V
28	209	6.0	918	2 S23377	collagen alpha 2(V
29	205	5.9	1028	1 CGHU1A	collagen alpha 1(V

30 205 5.9 1029 1 S21369 collagen alpha 2(V
31 204 5.8 13055 2 T16580 hypothetical prote
32 203.5 5.8 1170 2 S03308 cell surface glyco
33 203.5 5.8 1180 2 A35854 integrin alpha-1 c
34 200 5.7 238 2 C35243 collagen alpha 2(V
35 200 5.7 917 2 S09646 collagen alpha 2(V
36 200 5.7 1018 1 CGHU2A collagen alpha 2(V
37 195 5.6 1163 2 T56126 lymphocyte fuction
38 193 5.5 1151 2 A45226 integrin alpha-1 c
39 188.5 5.4 272 2 A55348 integrin alpha-1 -
40 187.5 5.4 1170 2 T45914 integrin alpha 2 s
41 184.5 5.3 643 2 T19549 hypothetical prote
42 182.5 5.2 1181 2 A33998 integrin alpha-2 c
43 178 5.1 763 2 T50807 complement factor
44 171 4.9 712 2 A45638 immunodominant mic
45 170.5 4.9 1178 2 S44142 VLA-2 protein homo

ALIGNMENTS

RESULT 1

A40020

collagen alpha 1(XII) chain precursor - chicken

N:Alternate names: fibrochimerin

C:Species: Gallus gallus (Chicken)

C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 15-Sep-2003

C:Accession: A40020; A34485; B3485; A28037; S23814; S22254; S28811

R:Yamagata, M.; Yamada, K.M.; Yamada, S.S.; Shinomura, T.; Tanaka, H.; Nishida, Y.; Obar

J. Cell Biol. 115, 209-221, 1991

A:Title: The complete primary structure of type XII collagen shows a chimeric molecule w
nous region of type IX collagen, and short collagenous domains with an Arg-Gly-Asp site.

A:Reference number: A40020; MUID:92011862; PMID:1918137

A:Accession: A40020

A:Molecule type: mRNA

A:Residues: 1-3124 <YAM>

A:Cross-references: GB:D00824; NID:G222810; PIDN:BA00701.1; PID:G222811

A>Note: in the authors' translation residues 1216-1219 are shown after residue 1235 and,

R:Gordon, M.K.; Gerecke, D.R.; Dublet, B.; van der Rest, M.; Olsen, B.R.

J. Biol. Chem. 264, 19772-19778, 1989

A:Title: Type XII collagen. A large multidomain molecule with partial homology to type I

A:Reference number: A34485; MUID:90062079; PMID:2584192

A:Accession: A34485

A:Molecule type: mRNA

A:Residues: 2456-2758, 'A', 2760-2802, 'F', 2804-2976, 'F', 2978-3124 <GOR>

A:Cross-references: EMBL:J05137; NID:G211284; PIDN:AAA48635.1; PID:G211285

A:Accession: B34485

A:Molecule type: protein

A:Residues: 2772-2792;2846-2873 <GOR2>

R:Gordon, M.K.; Gerecke, D.R.; Olsen, B.R.

Proc. Natl. Acad. Sci. U.S.A. 84, 6040-6044, 1987

A:Title: Type XII collagen: distinct extracellular matrix component discovered by cDNA c

A:Reference number: A28037; MUID:87317590; PMID:3476925

A:Accession: A28037

A:Molecule type: mRNA

A:Residues: 2960-2976, 'F', 2978-3074, 'AG', <GOR3>

A:Cross-references: EMBL:M17375; NID:G211649; PIDN:AAA48718.1; PID:G211650

A>Note: this sequence has been revised in reference A34485

R:Koch, M.; Bernasconi, C.; Chiquet, M.

Eur. J. Biochem. 207, 847-856, 1992

A:Title: A major oligomeric fibroblast proteoglycan identified as a novel large form of

A:Reference number: S23814; MUID:92362621; PMID:1323460

A:Accession: S23814

A:Molecule type: protein

A:Residues: 'X', 1333, 'Q', 1335-1347;1914-1928;2504, 'X', 2506, 'X', 2508-2511, 'X', 2513-2517 <

R:Dublet, B.; van der Rest, M.

J. Biol. Chem. 262, 17724-17727, 1987

A:Title: Type XII collagen is expressed in embryonic chick tendons. Isolation of pepsin-

A:Reference number: S22254; MUID:88087065; PMID:3121603

A:Accession: S22254

A:Molecule type: protein

A:Residues: 2831-2832, 'T', 2834, 'R', 2836-2843;3002-3014 <DUB>

R:Trueb, J.; Trueb, B.

	Matches	129;	Conservative	80;	Mismatches	178;	Indels	61;	Gaps	9;
Qy	273	EELSTOSLEPVSIGDPNCK---	IDLSFLIDGTSISIGKRFRIOKQLLADVAQAALDIGPAG	329	:	:	:	:	:	:
Dd	19	QALCSPLAQPOSEGH-LCTRPTDLV	FVVDSSRSVPVEFEKVFLSQVIESLDVGNA	77	:	:	:	:	:	:
Qy	330	PLMGVVVOYGDNPATHNLKTHNSRDL	KTAIEKITORGGLSNNGRAISFVTKNFFSKANG	389	:	:	:	:	:	:
Dd	78	TRGVWNYASTVKQEFSLAHVSKAALLQ	AVRRIQPLSTGTMTGLAIQPAITKAFGDAEG	137	:	:	:	:	:	:
Qy	390	NRSGAN- - - VVVWYDGHTDKVEASRL	ARESGINIFITTEGAENE--KQYVVBPEN	444	:	:	:	:	:	:
Dd	138	GRSRSPDIKWIVTVTDEGPQDSVSAR	ASGYELFAIGV-GSVDKATLRQIASEPQ	196	:	:	:	:	:	:
Qy	445	FANKAVCRITNGFYSLHVSQFWGLHKTL	QP-----LVKRCVCDTRLCACTCLNS----	493	:	:	:	:	:	:
Dd	197	DEHVD-----YVESYSVIEKLRSKPQR	AFCVVSDLCATGDHDCEQCVCSSPGSYT	246	:	:	:	:	:	:
Qy	494	-----ADIGPFVIDGSSSVGTGNFTVLQ	FVFNLTKEPE	526	:	:	:	:	:	:
Dd	247	CACHEGPTLNSDKTCNVCSGGGSATDL	VFLIDGSKSVRPENFELVKFKFSIQIVDTLD	306	:	:	:	:	:	:
Qy	527	ISTDTRIGAVOYTYBQRLEPGDPKYSKPD	ILNALKRVGYWSGGTSGAAINFALLEQLP	586	:	:	:	:	:	:
Dd	307	VSDKLAQVGLVQYSSSVSRQEPFLGRPHTK	IKDIIKAAVRNMSYMEKGTMWTGAALKYLIDNSP	366	:	:	:	:	:	:
Qy	587	KKS---KPKRKLMILLITGRSDVDVRI	PANMAHLKGVITYAICVAAAQEELEVIATHP	643	:	:	:	:	:	:
Dd	367	TVSSGARPGAQKGVIFTDGRSODYINDAAKT	AKOLGRTMPAVGVGNVAVEDELREIASEP	426	:	:	:	:	:	:
Qy	644	ARDHSFPVDFDNLHVYPRIIGNICTE	671	:	:	:	:	:	:	:
Dd	427	VAEHYFTTADFKTINOIGKKLKICV E	454	:	:	:	:	:	:	:

cartilage matrix protein precursor - chicken
C:Species: Gallus gallus (Chicken)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 28-Jul-2003
C:Accession: A33809; A26364
R:Kiss, I.; Deak, P.; Holloway Jr., R.G.; Dellus, H.; Mebust, K.A.; Frimberger, J. Biol. Chem. 264, 8126-8134, 1989
A:title: Structure of the gene for cartilage matrix protein, a modular protein
A:grins, von Willebrand factor, complement factors B and C2, and epidermal growth
A:Reference number: A33809; MUID:89255246; PMID:2542265
A:Accession: A33809
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <KIS>
A:Cross-references: GB:X12346; GB:X12347; GB:X12348; GB:X12349; GB:X12350; GB:X
R:Argaves, W.S.; Deak, F.; Sparks, K.J.; Kiss, I.; Goetinck, P.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 464-468, 1987
A:title: Structural features of cartilage matrix protein deduced from cDNA.
A:Reference number: A26364; MUID:87092429; PMID:3025875
A:Accession: A26364
A:Molecule type: mRNA
A:Residues: 78-493 <ARG>
A:Cross-references: GB:M14792; NID:g211545; PIDN:AAA48695.1; PID:g211546
C:Superfamily: matrilin; EGF homology; von Willebrand factor type A repeat homo
F:37-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F:225-260/Domain: EGF homology <EGF>
F:270-434/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 14.0%; Score 490; DB 2; Length 493;
Best Local Similarity 29.6%; Pred. No. 4e-25;
Matches 125; Conservative 68; Mismatches 177; Indels 52; Gaps 7;
QY 293 DL\$FLDGGT\$TGKRRFRIQKOLLADVAODLIGPAGPLMGVQYQGNP\$ATHENL\$KTHYN 352
DB 39 DLVFIIDSR\$SVNPQ\$EKKVFL\$SVIGL\$DVGPN\$TRGVIN\$YASAVKNE\$SLKTHQT 98
QY 353 SRLDKTA\$IKETQ\$RGSL\$NVGRAIS\$FVTKN\$P\$SKANGN\$SGAPN\$-\$\$\$VVWVDG\$HPTDK 409

353 SRDLKTAIEKTIQRGGLSNVGRAISFTVKIPFSKANGNRSCAPN---WWWVVDGWPDK 409

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Db 99 KAELLQAVQRIEPLSTGTMGLAIQFAISRAFSDETEGARLSRNKVAIVTIDGRPDQG 158
QY 410 VEEASRLARESGINIFFI-----TIEGAARENEKQYVVEPNFANK---AV 450
Db 159 VQDVSAARQAGIEIFAIGVGRVDMHTLRQIASEPLDHRVDHYVESYVIEKLTHTKQEPAP 218
QY 451 C-----RTNGFYSLHVOSWFLGKHTLQLOPKVRVCDTDLRACSKTCLN 492
Db 219 CVVSDLCATGDHDCQICISTPGSYKCACKBGGTFLAND-----GKTCS-----ACSGSGS 269
QY 493 SADIGFVIDGSSSVGTGNFRVLQFVTLNLTQVTKBPEISDTDRIGAVQVYVQRLPEFGDKY 552
Db 270 ALDLVFLIDGSKSVRPNFELVKKFINQIVESLEVEKQAGVGLVQYSSSVRQEPFLQGF 329
QY 553 SSKPDILNAIKRYGYMSGTSTGAANFALEQLF---KKSPPKPKMLMILITDGRSYDDV 609
Db 330 KNKKDIAKAAVKMAYMEKGTMTGQALKYLVDSFSFANGARPGVPKVGIVFTDGRSQDYI 389
QY 610 RIPAMAAHLKGVITYAIGVAAQAQBELEVIATIPADHSPFVDFPNLHQYVPRITQNIC 669
Db 390 TDAAKKAKDLGPRMFAVGNAVEDELREITASBPVAHYFTYADPRTISNIGKKLQMKIC 449
QY 670 TE 671
Db 450 VE 451

RESULT 5
S66522
catilage matrix protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 28-Jul-2003
C;Accession: S66522
R;Azodi, A.; Hauser, N.; Studer, D.; Paulsson, M.; Hiripi, L.; Bosze, Z.
Eur. J. Biochem. 236, 970-977, 1996
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein
A;Reference number: S66522; MUID:96270751; PMID:8665920
A;Accession: S66522
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-500 <AS2>
A;Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179
C;Genetics:
A;Gene: CMP
C;Superfamily: matrilin; EGF homology; von Willebrand factor type A repeat homology
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-500/Product: cartilage matrix protein #status predicted <MAT>
F;43-210/Domain: von Willebrand factor type A repeat homology <VWA1>
F;231-266/Domain: EGF homology <EGF>
F;277-441/Domain: von Willebrand factor type A repeat homology <VWA2>

Query Match 14.0%; Score 490; DB 2; Length 500;
Best Local Similarity 28.8%; Pred. No. 4.1e-25;
Matches 130; Conservative 72; Mismatches 184; Indels 66; Gaps 8;

QY 266 SLGLVPKKELSQSLSPVSLGDPNCKTDLSPFLIDGTSIGKRRPRIQKQLLADVAAQALDI 325
Db 27 SLSLVPQPRGHCKTRPT-----DLVFWVDSRSSRVPVEPKVKVFLSQVIESLDV 77

QY 326 GPAGPLMGVVOYGDNPATFNKHTNSRDLKTAIEKLTORGGLSNVGRALSPVTKNFFS 385
Db 78 GPNATRVGLVNYASTVKPEPFLRAHGSKASLLQAVRRIQPLSTGTGTMGLAQFAITKALS 137

QY 386 KANGNRSAPN---VVVMVDGWFTDVEASRLARESGINIFITTEGAARENE--KQYV 440
Db 138 DAEGGRARSPIISKVIVVTDGRPDQSDVRDSEARASGIELFAIGL-GRVDRATLRQIA 196

QY 441 VEPNFAKAVCRNGFYSLHVQSWFGLHKTLP-----LVKRVCDTDLRACSKTCLNS- 493
Db 197 SEPODEHVD-----YVESYNTVIEKAKKQFAFCVVSQDLCATGDHDCBOLCVSSP 246
QY 494 -----ADIGFVIDGSSSVGTGNFRVLQFVTNLT 522
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Db 247 GSYTCACHEGFTLNSDKTCNVCRCGGSGSATDLVFLIDGSKSVRPNFELVKKFINQIV 306
QY 523 KEFEISDTDRIGAVQVYVQRLPEFGDKYSSKPDILNAIKRYGYMSGGTTGTAANFAL 582
Db 307 DTLDVDRLAQVGLVQYSSSIRQEPFLGRFHSKKDIKARVRNMSYMEKGTMTGAALKYLI 366
QY 583 BQLPKKS---KPKRKRLMILITDGRSYDDVRIIPAMAAHLKGVITYAIGVAAQAQBELEVI 639
Db 367 DNSFTVSSGARPGQAKGVIVFTDGRSQDYINDAARAKDLGPKMFAVGVGNAVEEELREI 426
QY 640 ATPHARDHSPFVDFPNLHQYVPRITQNICTE 671
Db 427 ASEPVADHYFTYADPRTINQIGKKLQKQICVE 458

RESULT 6
CGHU3A
collagen alpha 3(VI) chain precursor [validated] - human
N;Contains: collagen alpha 3(VI) chain, splice form A9/N10(-)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 12-Nov-1999 #text_change 15-Sep-2003
C;Accession: A59140; S13679; S24465; A57083; S28776; S00245; C31952; C29848; S26510; S4;
R;Chu, M.L.
submitted to GenBank, May 1998
A;Reference number: A59140
A;Accession: A59140
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-3176 <CHU>
A;Cross-references: GB:X52022; NID:g3127925; PIDN:CAA36267.1; PID:g3127926
R;Chu, M.L.; Zhang, R.Z.; Pan, T.; Stokes, D.; Conway, D.; Kuo, H.J.; Glanville, R.; Ma;
EMBO J. 9, 305-393, 1990
A;Title: Mosaic structure of globular domains in the human type VI collagen alpha-3 chain
itors.
A;Reference number: S13679; MUID:90151612; PMID:1689238
A;Accession: S13679
A;Molecule type: mRNA
A;Residues: 1-30,237-313, 'CWV', 318-322, 'AR', 326-1815, 'PD', 1818-1819, 'ID', 1822-3176 <CHS>
A;Cross-references: EMBL:X52022; NID:g3127925
A;Accession: S24465
A;Molecule type: protein
A;Residues: 574-585; 965-973, 'X', 975-976; 1306-1325; 1361-1377; 1381-1401; 1473-1506, 'X', 1501-1962, 'X', 1964-1965; 2018-2037; 2374-2410; 2445-2459; 2466-2469, 'X', 2471-2474; 2504-2508, 'X',
R;Zanussi, S.; Doliana, R.; Segat, D.; Bonaldo, P.; Colombatti, A.
J. Biol. Chem. 267, 24082-24089, 1992
A;Title: The human type VI collagen gene. mRNA and protein variants of the alpha3 chain
A;Reference number: S28776; MUID:93054780; PMID:1339440
A;Accession: A57083
A;Molecule type: DNA
A;Residues: 310-328 <ZAN>
A;Accession: S28776
A;Molecule type: mRNA
A;Residues: 32-126, 'AK', 129-136, 'L', 138-236 <ZA2>
A;Cross-references: GB:S49432; NID:g260296; PIDN:AAB24261.1; PID:g260297
R;Chu, M.L.; Mann, K.; Deutzmann, R.; Pribula-Conway, D.; Hsu-Chen, C.C.; Bernard, M.P.
Eur. J. Biochem. 168, 309-317, 1987
A;Title: Characterization of three constituent chains of collagen type VI by peptide se
A;Reference number: S00126; MUID:88029444; PMID:3665927
A;Accession: S00245
A;Molecule type: mRNA; protein
A;Residues: 2024-2046; 2092-2156, 'R', 2203-2208, 'X', 2210-2211, 'X', 2213-2227; 2228-2251; 2311
A;Cross-references: GB:X06196; NID:g30055; PIDN:CAA29557.1; PID:g1335034
R;Chu, M.L.; Conway, D.; Pan, T.; Baldwin, C.; Mann, K.; Deutzmann, R.; Timpl, R.
J. Biol. Chem. 263, 18601-18606, 1988
A;Title: Amino acid sequence of the triple-helical domain of human collagen type VI.
A;Reference number: A31952; MUID:89066644; PMID:3198591
A;Accession: C31952
A;Molecule type: mRNA
A;Residues: 2038-2373 <CH4>
A;Cross-references: GB:J04211; GB:M20778
A;Note: parts of this sequence were determined by protein sequencing
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Db 713 IVGTTAIPPT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETSS 757
Qy 228 ---LWSTATTSSQNR-----PRADPGIQQDPGSAAFQKPVGADVSLGLVPKEELS 276
Db 758 LRVVWDISDHNAQQFVTVLTAKGDRABEAIMVPGRQNTLLQP-----LLPDTYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDLSPIDGSTSIGKRRFRIQKQLADVAQALDIGPAGP 330
Db 810 VTIITPIYADGEGVSAGPKTLP-----APNLRVSDWYNNRLRISMD-APPSP 859
Qy 331 LAG--VVQYGDN---PATHFNKTHNSRDLKTAIEKIQORGLSNVGRASIVPTKNFES 385
Db 860 TMGYRIVYKSIINVPGA---LFTFVG-DINTIL-----ILNLFSGTETYSVKVPAS 906
Qy 386 KANG---NRSGAPNVVWVDGHPDTKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTGVAKTLYLVGNLDTVQVRMTSLCAQMLHRHATAYRVVIESLVGKKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTLO----- 472
Db 966 --EVNLGG-GVPR-HCFPELMPGTEYKISVHAQLOEIEGPAVSIMETTLPPPTPTSPS 1021
Qy 473 -----PLVKRVCTDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNTLKE 524
Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDGWSIGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTTRIGAVQVYTEORLEFGPKYSSKPDILNAIKRVGVWSGTTSGAAINFALE 583
Db 1072 LDKIGDGTQVVAIQSDDPTEFKLNAYTKETLLEAIQOIAYKGGNTKGAIKHARE 1131
Qy 584 QLF-----KSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVIITVAIGVAMAAOELE 637
Db 1132 VLFTGAGMRKGP--KVLVWITDGRSQDDVNVKVSREMQLDGFSPFAIGVADADYSELV 1188
Qy 638 VIATHPARDSPPVDFEDNLHQVPRILQNIC 669
Db 1189 NIGSKPSERHVPFVDDPDAFTKIEDELITFVC 1220
RESULT 8
S78476
collagen alpha 1(XIV) chain precursor, long form - chicken
C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Sep-2003
C;Accession: S78476; S31211
R;Trueb, B.
submitted to the EMBL Data Library, January 1993
A;Reference number: S78476
A;Accession: S78476
A;Molecule type: mRNA
A;Residues: 1-1888 <TRU>
A;Cross-references: EMBL:X70793; NID:q288872; PIDN:CAA50064.1; PID:q288873
R;Maechli, C.; Trueb, J.; Kessler, B.; Winterhalter, K.H.; Trueb, B.
Eur. J. Biochem. 212, 483-490, 1993
A;Title: Complete primary structure of chicken collagen XIV.
A;Reference number: S31211; MUID:93185668; PMID:8444186
A;Accession: S31211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416;1460-1811,1843-1888 <WAE>
A;Cross-references: EMBL:X70793
C;Genetics:
A;Gene: Col14A1
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-1888/Product: collagen alpha 1(XIV) chain, long form #status predicted <MAT>
F;29-110/Domain: fibronectin type III repeat homology <FN3A>
F;156-320/Domain: von Willebrand factor type A repeat homology <VWA1>
F;352-433/Domain: fibronectin type III repeat homology <FN3B>
F;442-525/Domain: fibronectin type III repeat homology <FN3C>
F;534-614/Domain: fibronectin type III repeat homology <FN3D>
F;623-707/Domain: fibronectin type III repeat homology <FN3E>

F;741-823/Domain: fibronectin type III repeat homology <FN3P>
F;832-914/Domain: fibronectin type III repeat homology <FN3G>
F;922-1009/Domain: fibronectin type III repeat homology <FN3H>
F;1040-1205/Domain: von Willebrand factor type A repeat homology <VWA2>
Query Match 9.5%; Score 331; DB 2; Length 1888;
Best Local Similarity 24.8%; Pred. No. 1.4e-13;
Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;
Qy 174 IFGTTAIPPT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETSS 757
Db 713 IVGTTAIPPT-----VTTTTTATTPKPTIAVFR-----GVRNLVIDDETSS 757
Qy 228 ---LWSTATTSSQNR-----PRADPGIQQDPGSAAFQKPVGADVSLGLVPKEELS 276
Db 758 LRVVWDISDHNAQQFVTVLTAKGDRABEAIMVPGRQNTLLQP-----LLPDTYK 809
Qy 277 TQSL-----EPVSLGDPNCKIDLSPIDGSTSIGKRRFRIQKQLADVAQALDIGPAGP 330
Db 810 VTIITPIYADGEGVSAGPKTLP-----APNLRVSDWYNNRLRISMD-APPSP 859
Qy 331 LAG--VVQYGDN---PATHFNKTHNSRDLKTAIEKIQORGLSNVGRASIVPTKNFES 385
Db 860 TMGYRIVYKSIINVPGA---LFTFVG-DINTIL-----ILNLFSGTETYSVKVPAS 906
Qy 386 KANG---NRSGAPNVVWVDGHPDTKVEASRLAR---ESGINIFITIEGAENKQY 439
Db 907 YSTGFSDALTGVAKTLYLVGNLDTVQVRMTSLCAQMLHRHATAYRVVIESLVGKKQ- 965
Qy 440 VVEPNFANKAVCTNGFYSL--HVQSWFGLHKTLO----- 472
Db 966 --EVNLGG-GVPR-HCFPELMPGTEYKISVHAQLOEIEGPAVSIMETTLPPPTPTSPS 1021
Qy 473 -----PLVKRVCTDRLACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNTLKE 524
Db 1022 TTLPPPTIPPAKEVCKAAK-----ADLVFLVDGWSIGDDNFNKIISFLYSTVGA 1071
Qy 525 FE-ISTDTTRIGAVQVYTEORLEFGPKYSSKPDILNAIKRVGVWSGTTSGAAINFALE 583
Db 1072 LDKIGDGTQVVAIQSDDPTEFKLNAYTKETLLEAIQOIAYKGGNTKGAIKHARE 1131
Qy 584 QLF-----KSKPNKRKLMILITDGRSYDDVRIPAMAAHLKGVIITVAIGVAMAAOELE 637
Db 1132 VLFTGAGMRKGP--KVLVWITDGRSQDDVNVKVSREMQLDGFSPFAIGVADADYSELV 1188
Qy 638 VIATHPARDSPPVDFEDNLHQVPRILQNIC 669
Db 1189 NIGSKPSERHVPFVDDPDAFTKIEDELITFVC 1220
RESULT 9
A54849
collagen alpha 1(VII) chain precursor - human
N;Alternate names: procollagen alpha 1(VII) chain
C;Species: Homo sapiens (man)
C;Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 15-Sep-2003
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Utito, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alpha 1(VI
A;Reference number: A54849; MUID:94327588; PMID:8051117
A;Accession: A54849
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2944 <CHR>
R;Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
Biochem. Biophys. Res. Commun. 183, 958-963, 1992
A;Title: Molecular cloning and characterization of type VII collagen cDNA.
A;Reference number: PH0844; MUID:92231902; PMID:1567409
A;Accession: PH0844
A;Molecule type: mRNA
A;Residues: 'BFR', 340-475, 'RALSTASHSTLCNRAWRHPCNRGSHWTRAAACEPCNRPASHRAADAG', 524-528, 'C'.

A:Cross-references: DDBJ:D11152; DDBJ:D13694; NID:G453698; PIDN:BA02853.1; PID:G453699
A:Experimental source: keratinocyte
A:Note: The authors translated the codon ACC for residues 394 and 397 as Tyr
R:Parente, M.G.; Chung, L.C.; Rynnaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat
Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A:Title: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene.
A:Reference number: S16316; MUID:91334380; PMID:1871109
A:Accession: S16316
A:Molecule type: mRNA
A:Residues: 815-892, 'E', 894-1439 <PAR>
A:Cross-references: GB:M65158; GB:G49017; NID:G180914; PIDN:AAA96439.1; PID:G180915
A:Experimental source: keratinocyte
R:Gammon, W.R.; Abernathy, M.L.; Padilla, K.M.; Prisyayanh, P.S.; Cook, M.E.; Wright, J.
J. Invest. Dermatol. 99, 691-696, 1992
A:Title: Noncollagenous (NC1) domain of collagen VII resembles multidomain adhesion prot
A:Reference number: 156328; MUID:93107742; PMID:1469284
A:Accession: 156328
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 'EPR', 372-517, 'DV', 520-540, 'W', 542-1255 <RES>
A:Cross-references: GB:S51236; NID:G262308; PIDN:AA824637.1; PID:G262309
R:Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgess, R.E.
J. Biol. Chem. 264, 3822-3826, 1989
A:Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagen
A:Reference number: A30296; MUID:89139437; PMID:2537292
A:Accession: A30296
A:Molecule type: protein
A:Residues: 'A', 1240-1246, 'G', 1248-1250, 'XE', 1253-1255, 'Q', 1257, 'E', 2032, 'C', 2034-2041,
A:Note: two reported peptides cannot be reliably located
R:Greenpan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
A:Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A:Reference number: 148103; MUID:93271985; PMID:8499916
A:Accession: 148103
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 2395-2871, 'S', 2873-2944 <RES>
A:Cross-references: GB:L06862; NID:G388713; PIDN:AAA89196.1; PID:G388714
R:Christiano, A.M.; Rynnaenen, J.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A:Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser sub
A:Reference number: A55255; MUID:94224777; PMID:8170945
A:Contents: annotation
A:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Genetics:
A:Gene: GDB:COL7A1; EBR1; EBD1; EB
A:Cross-references: GDB:128750; OMIM:120120
A:Map position: 3p21.3-3p21.3
A:Note: defects in this gene can result in dominant and recessive dystrophic epidermolys
A:Note: there are 118 introns
C:Complex: type VII collagen is probably a homotrimer
C:Function:
A:Description: structural component of extracellular polymer associated with anchoring f
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F:17-1253/Domain: amino-terminal nonhelical #status predicted <NC1>
F:36-201/Domain: von Willebrand factor type A repeat homology <VWA1>
F:231-318/Domain: fibronectin type III repeat homology <FN1>
F:327-413/Domain: fibronectin type III repeat homology <FN2>
F:414-502/Domain: fibronectin type III repeat homology <FN3>
F:508-593/Domain: fibronectin type III repeat homology <FN4>
F:598-683/Domain: fibronectin type III repeat homology <FN5>
F:686-771/Domain: fibronectin type III repeat homology <FN6>
F:776-862/Domain: fibronectin type III repeat homology <FN7>
F:864-952/Domain: fibronectin type III repeat homology <FN8>
F:954-1045/Domain: fibronectin type III repeat homology <FN9>
F:1052-1219/Domain: von Willebrand factor type A repeat homology <VWA2>
F:1170-1172/Region: cell attachment (R-G-D) motif
F:1189-1253/Region: cysteine/proline-rich
F:1254-2783/Region: interrupted helical
F:1334-1336/Region: cell attachment (R-G-D) motif

F:2008-2010/Region: cell attachment (R-G-D) motif
F:2553-2555/Region: cell attachment (R-G-D) motif
F:2784-2944/Domain: carboxyl-terminal nonhelical #status predicted <NC2>
F:2876-2929/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
F:337, 786, 1109/Binding site: carboxylate (Asn) (covalent) #status predicted
F:2167, 2176, 2185, 2188, 2664, 2667, 2673/Modified site: 4-hydroxyproline (Pro) #status exper
F:2625, 2631/Modified site: 5-hydroxylysine (Lys) #status experimental
F:2625, 2631/Binding site: carboxylate (Lys) (covalent) #status experimental
F:2634, 2802, 2804/Disulfide bonds: interchain #status predicted
Query Match 9.4%; Score 329.5; DB 2; Length 2944;
Best Local Similarity 35.7%; Pred. No. 3 4e-13;
Matches 80; Conservative 37; Mismatches 88; Indels 19; Gaps 4;
QY 470 TLQPLKRVVC-----DTRLACSKTCLNSADIGFVIDGSSVGTGNFTVLQ 516
DB 2 TLRLVAALCAGILAEAPRVAQRHRTVCTR--LYAADIVFLDGGSSIGRSNPREVAS 59
QY 517 FVTNLTKEFE--ISDTDTTRIGAVQVYTBQLEFGDFKYSKPDILNAIKRVGWSGTST 574
DB 60 FLEGLVLPFSGAASAGQVRFPATVQVSDPRTFGLDGLSGGSDVIRAIRELSTKGNVTR 119
QY 575 GAAINPFALEOLF--KSKSPNKKRKLMLITDGRSYDDVRIPANAAHLKGVIITVAIGVAA 632
DB 120 GAAILHVADHVLPLQARPGVPKVCILLITDGSQDLVDTAQRLKQGVKLVFAVGIKNAD 179
QY 633 QEELEVIATHPARDHSFFVDFDNLHQVPRITQICTEFNSOP 676
DB 180 PEELKRVASQPTSDPFPPFVNDPSILRTLPLVSRVCTTAGGVP 223
RESULT 10
A45974
N:Alternate names: undulin
C:Species: Gallus gallus (chicken)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Sep-2003
R:Accession: A45974; S30085; S22916; S17035; S20833
R:Gerecke, D.R.; Foley, J.W.; Castagnola, P.; Gennari, M.; Dublet, B.; Cancedda, R.; Lin
J. Biol. Chem. 268, 12177-12184, 1993
A:Title: Type XIV collagen is encoded by alternative transcripts with distinct 5' region
na.
A:Reference number: A45974; MUID:93280195; PMID:8505337
A:Accession: A45974
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-1747 <GER>
A:Experimental source: embryo skin
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:133364, NCBI:133365)
R:Apte, S.S.
submitted to the EMBL Data Library, March 1992
A:Reference number: S30085
A:Accession: S30085
A:Molecule type: mRNA
A:Residues: 1472-1660 <APT>
R:Cross-references: EMBL:X65122; NID:G62871; PIDN:CAA46238.1; PID:G9938175
R:Trueb, J.; Trueb, B.
Eur. J. Biochem. 207, 549-557, 1992
A:Title: Type XIV collagen is a variant of undulin.
A:Reference number: S22916; MUID:92339443; PMID:1339349
A:Accession: S22916
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 286-494, 'Q', 496-834, 'A', 836-1119, 'KL', 1122-1402, 1409-1439 <TRU>
R:Gordon, M.K.; Castagnola, P.; Dublet, B.; Linsemayer, T.F.; van der Rest, M.; Mayne, R.
Eur. J. Biochem. 201, 333-338, 1991
A:Title: Cloning of a cDNA for a new member of the class of fibril-associated collagens
A:Reference number: S17035; MUID:92037585; PMID:1935930
A:Accession: S17035
A:Molecule type: mRNA
A:Residues: 1472-1659 <GOR1>
A:Accession: S20833

A;Molecule type: protein
A;Residues: 1551-1570;1593-1599;1639-1667 <GOR2>
C;Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trimer
F;40-204/Domain: von Willebrand factor type A repeat homology <VWA1>
F;236-317/Domain: fibronectin type III repeat homology <FN3A>
F;326-409/Domain: fibronectin type III repeat homology <FN3B>
F;418-498/Domain: fibronectin type III repeat homology <FN3C>
F;507-591/Domain: fibronectin type III repeat homology <FN3D>
F;625-707/Domain: fibronectin type III repeat homology <FN3E>
F;716-798/Domain: fibronectin type III repeat homology <FN3F>
F;806-893/Domain: fibronectin type III repeat homology <FN3G>
F;924-1089/Domain: von Willebrand factor type A repeat homology <VWA2>
F;1111-1352/Domain: non-collagenous NC4 #status predicted <NC4>
F;1511-1553/Domain: non-collagenous NC2 #status predicted <NC2>
F;1554-1659/Domain: triple helical domain COL1 #status predicted <COL1>

Query Match 9.48; Score 329; DB 2; Length 1747;
Best Local Similarity 24.8; Pred. No. 1.7e-13;
Matches 142; Conservative 74; Mismatches 216; Indels 140; Gaps 24;

QY 174 IPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSEMD----- 227
DB 597 IVGTAPPT-----VTTTTTTTATPKPTIAVFT-----GVRLVIDDETSS 641

QY 228 ---LWSTATTSSNR-----PRADPGIQRDPGSAAPQKPVGADVSLGLVPKEELS 276
DB 642 LRVVWDISDHAQFRVYTLTAKGDRAEAIMVGRQNTLLQP-----LLPDTYK 693

QY 277 TQSL-----EPVSLGDPNCKIDISFLIDGSTSGKRRFRIOKLLADVAQALDIPAGP 330
DB 694 VTTPIVADGEGSVSAPGKTLPLS-----APNLRVSDWYRLRISWD-APPSP 743

QY 331 LMG---VVQYGDN---PATHFNKLTHTNSRDLKTAIEKITQRGGLSNVGRASIFVTKNFFS 385
DB 744 TMGVRIYKSNVPGPA---LETFVGD-DINTIL-----ILNLPSTGYSVKVPAS 790

QY 386 KANG---NRSGAPNVVVMVDGWTDKVBEASRLAR---ESGINIPITIEGAENKQY 439
DB 791 YSTGFSDALAGVAKTLVGLVNTLDYQVRMTSLCAQWQLHRHATRYRWVIESLVGKKQ- 849

QY 440 VVEPNFANKAVCTNGFVSL---HVQSWFLGHLTKLQ----- 472
DB 850 ---EVNLGG-GVPR-HCFPELPGTGYEKISVHAQLEIGEPASVIMETTLFPPTQPTSPS 905

QY 473 -----PLVXRVCDTDLRLCAKSTCLNSADIGFVIDGSSVGTGNFRTVLQVFNLTKE 524
DB 906 TTLPPPTIPPAKCVCKAAK-----ADLVFLVDGWSIGDNNFNKLIISFLYSTVGA 955

QY 525 FB-ISDTRIGAVQVYTBORLEFGPKYSSKPDILNAIKRVGYWSGTSTGAAINFALE 583
DB 956 LDKIGPDGTVAITQFSDDPRTPEKLNAYKTETLLEAIQQIAYKGGNTKTKAKHARE 1015

QY 584 QLF-----KSKENKPKMLITIDGRSYDDVRIPAMAHLKGVITVIAIGVAMAAQEELE 637
DB 1016 VLFTEAGMRGIP---KVLVITIDGRSQDDVNKVSREMQLDGFSFPAIGVADADYSELV 1072

QY 638 VIATHPRDHSFFVDEFDNLHQVYPRITQNIC 669
DB 1073 NIGSKPSERHVFVDDFDAFTKIEDELITFVC 1104

RESULT 11
T28797
hypothetical protein C16E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28797
R;Geisel, C.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid C16E9.
A;Reference number: Z20525
A;Accession: T28797
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-567 <GB1>
A;Cross-references: EMBL:U39677; PIDN:AAC47957.1; GSPDB:GN00028; CESP:C16E9.1
A;Experimental source: strain Bristol N2; clone C16E9
C;Genetics:
A;Gene: CESP:C16E9.1
A;Map position: X
A;Introns: 15/3; 77/3; 132/1; 185/3; 231/1; 271/2; 301/2; 430/3; 509/1

Query Match 9.08; Score 314.5; DB 2; Length 567;
Best Local Similarity 22.08; Pred. No. 3e-13;
Matches 130; Conservative 84; Mismatches 213; Indels 163; Gaps 20;

QY 172 PPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSP-SAASTTSIPRQSVGHRSEMDLWS 230
DB 37 PMP-----PTDPPGYPDSTFTDTPTTAPPSSNGULRAPPMPCWT 75

QY 231 TATYTSSNRP-----RADPGIQRDPGSAAPQKPVGADVSLGLVPKEELSTQSL 280
DB 76 QETPKSSGQOLKIEDVWVGNNDISHVEEVNGSGDTEGSGDGKSTESPDASGEA 135

QY 281 EPVSLGD-----PNCKIDLSFLIDGSTSGKRRFRIOKLLADVAQALDIP 327
DB 136 QGDSLPDIMKAMDSEAEVLGVNCPSDIIFVIDATSSV-RGIFEQVITYIEKVVLEGLDVP 194

QY 328 AGPLMGVVQYGD---NPATFNKLTHTNSRDLKTAIEKITQRGGLSNVGRASIFVTKNFFS 385
DB 195 TVDHVGAIVYSSEKKQRTKIKLGEHDKDRGSLVKADELPPFSGITATQALKFAANH--- 251

QY 386 KANGNRSGAPNVVVMVDGWTDKVBEASRLARSEGINIPITIEGAENKQYVVEPNF 445
DB 252 -TEGRRENTLNVYLLTDGYSDILIESGARVLR-----VNS 288

QY 446 ANKAVCRTNGFYSLHVQSWFLGHLTKLQ-----PLVPR---VCDT----- 481
DB 289 A-----IYAVSIGRIP-LRKELEMITGNPNVLTGSMYGLVVKRLKLCDAIRKAA 338

QY 482 -----DRLACS-----KTCLNSADIGF 498
DB 339 TLKDSNPLVRPGFLSDRFQHRSLTANLEAKKHETEDFVKTPKRGVPKDCI---YDIGI 396

QY 499 VIDGSSVGTGNFRTVLQVFNLTKEFISDTRIGAVQVYTBORLEFGDKYSSKPD 558
DB 397 IPDSSGSL-EKNFQKQAFAPAKQLVEQMPISDNATRVGIVQAGTKVRLANFSPQKSQL 455

QY 559 LNAIKRVGYWSGTSTGAAINFALEQLPKSK-PNKRKMLILITDGRSYDDVRIPAMAHAH 617
DB 456 KTIIDRSPFYSGTFTTNOALK-KMAALVEESKRPNAKILKMLFTDGYSAEDTSEGEALK 514

QY 618 LKGVITVIAIGV-----AWAAQEELEVIATHPRDHSFPVDEFDNLHQVYP 662
DB 515 SQGVVVYTVGISTDKSAGLNNKELRGMAT--SSHHYDSSDFADLLKHFP 562

RESULT 12
T46488
hypothetical protein DKFZp34J065.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C;Accession: T46488
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23035
A;Accession: T46488
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-741 <AAA>
A;Cross-references: EMBL:AL137638
A;Experimental source: adult testis; clone DKFZp34J065
C;Genetics:
A;Note: DKFZp34J065.1

Query Match 8.54; Score 298; DB 2; Length 741;

[illegible]

A; Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146/1
C; Superfamily: von Willebrand factor type A repeat homology; EGF homologous; fibronectin
P; S12-679/Domains: von Willebrand factor type A repeat homology <WAL>
F; 754-793/Domain: fibronectin type II repeat homology <RFL>
F; 1201-1244/Domains: fibronectin type I repeat homology <EGF>

Query Match 8.0%; Score 279; DB 2; Length 3051;
Best Local Similarity 37.4%; Pred. No. 8.ee-10;
Matches 74; Conservative 37; Mismatches 73; Indels 14; Gaps 7;

QY 477 RVCDDRLACSKTCLNSADIGPVIDGSSVGTGNPRFT-VLQFYTNLTKEFEISDPTDRIG 535
| | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 500 RVC-TVQTTCPK---OKTDLVPLVDGGSGSIGSVFKNEVLRFVRBPFVELFGSKTRVG 555
|| || : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 536 AVQTYEORLEFGFDKYSKPDIINAIKRIVGYMSGCTGCIAINFALBQLFKK----SKPN 592
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 556 LIQSYDSQRHEFPDLDOYGDRUSLLKGISTEQYLTLTGTAALOHWVOGESRGARQP 615
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 593 K---RKGMILITDGSRDYDVRIPIAMAHLHGKITVAIGA--AAQQBELEVVIATHPARDHS 648
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 616 QSDIARVALIIITDCRSQNVTGPADSARKLSINTPAIGTVTHVLASELESAGSPNR--WW 673

QY 649 PFYDFDNHLYVPRIIQ 666
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 674 FYDKFKOLDTRLASMIQ 691

RESULT 15
WMU
von Willebrand factor precursor - human
C; Species: Homo sapiens (man)
C; Date: 04-Dec-1986 #sequence revision 30-Jun-1993 #text change 22-Jun-1999
A; Accession: A34480; S02377; A37139; S23676; A25298; A25366; S23618; S23645; A94
R; Mancuso, D.J.; Tuley, B.A.; Westfield, L.A.; Worral, N.K.; Shelton-Inloes, B.B.; Sora
J. Biol. Chem. 264, 19514-19527, 1989
A; Title: Structure of the gene for human von Willebrand factor.
A; Reference number: A34480; PMID:90062044; PMID:2584182
A; Accession: A34480
A; Molecule type: DNA
A; Residues: 1-2813 <MAN>
A; Cross-references: EMBL:M25864
R; Bonthonron, D.; Orkin, S.H.
Eur. J. Biochem. 171, 51-57, 1988
A; Title: The human von Willebrand factor gene. Structure of the 5' region.
A; Reference number: S02377; MUID:88111704; PMID:2828057
A; Accession: S02377
A; Molecule type: DNA
A; Residues: 1-177 <BO2>
A; Cross-references: EMBL:X06828
R; Mancuso, D.J.; Tuley, B.A.; Westfield, L.A.; Lester-Mancuso, T.L.; Le Beau, M.M.; Sora
Biochemistry 30, 253-269, 1991
A; Title: Human von Willebrand factor gene and pseudogene: structural analysis and differ
A; Reference number: A37139; MUID:91105089; PMID:1988024
A; Accession: A37139
A; Molecule type: DNA
A; Residues: 990-1947 <MAD>
A; Cross-references: GB:M60675; NID:g340357; PIDN:AABg1295.1; PID:g553810
A; Note: the authors translated the codon CGC for residue 156 as Glu
R; Collins, C.J.; Underdahl, J.P.; Levine, R.B.; Ravera, C.P.; Morin, M.J.; Donnalaglan, i
Proc. Natl. Acad. Sci. U.S.A. 84, 4393-4397, 1987
A; Title: Molecular cloning of the human gene for von Willebrand factor and identificatio
A; Reference number: S23676; MUID:87260814; PMID:3496594
A; Accession: S23676
A; Molecule type: DNA
A; Residues: 2731-2813 <COL>
A; Cross-references: EMBL:M16945
R; Bonthonron, D.; Orr, E.C.; Mitsock, L.W.; Ginsburg, D.; Handin, R.I.; Orkin, S.H.
Nucleic Acids Res. 14, 7125-7127, 1986
A; Title: Nucleotide sequence of pre-pro-von Willebrand factor cDNA.
A; Reference number: A25298; MUID:87016349; PMID:3489923
A; Accession: A25298
A; Molecule type: mRNA
A; Residues: 1-470, 'v', 472-2813 <BON>


```
Qy 427 ITIEGAENBKQYVVEP-----NFANKAVCRTNGFYSLHVQSWFGLHKTLOPL 474
Db 1399 RYVQGL--KKKKVIVFVGIGPHANLKQIRLIEKQAPENKAPVLSVDE---LEQORDEI 1453
Qy 475 VKRVCDDRLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
Db 1454 VSYLCDLAPEAPPPTLPHPMAQVTVGPGLLGVSTLGPKNENMVLDAFVLEGSCKIGEAD 1513
Qy 511 FRTVLQFVNTLTKFBISDTRIGAVQYTYEQRLFCGDKYSSKPDILNAIKRVGYWSG 570
Db 1514 FNRSKFPMEEVIQRMVQGDSDIHVTVLQYSYMTVEYFPESEAQSGDILQVRREIRYQGG 1573
Qy 571 G-TSTGRAINFALBQLKCKSKENKK---LMLITDGRSYDDV-RIPMAAHLKGVITYA 625
Db 1574 NRTWTGLALRYLSHSLVLSQDREQAPNLVYMTGNPASDEIRKLPG-----DIQVVP 1627
Qy 626 IGVAWAAQ-BELEVIATHPARDSFFVDFDNLHGYVPRIIQNIC 669
Db 1628 IGVGNANVQELERIGWPNA---PILIQDFETLPREAPDLVLQRC 1669
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Search completed: May 27, 2004, 16:47:36
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:42:02 ; Search time 60 Seconds
(without alignments)
3192.787 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502
Sequence: 1 MRTVLTWKASVIEFLVLL.....QYVPRIIQICTERNOPRN 678

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	3502	100.0	678	3 AAY66674	Aay66674 Membrane-
2	3502	100.0	678	4 AAU29098	Aau29098 Human PRO
3	3502	100.0	678	4 AAB87542	Aab87542 Human PRO
4	3502	100.0	678	4 AAB65197	Aab65197 Human PRO
5	3502	100.0	678	5 ABG95867	Abg95867 Human sec
6	3502	100.0	678	6 ABU58474	Abu58474 Human PRO
7	3502	100.0	678	6 ABU88022	Abu88022 Novel hum
8	3502	100.0	678	6 ABU84337	Abu84337 Human sec
9	3502	100.0	678	6 ABR66211	AbR66211 Human sec
10	3502	100.0	678	6 ABR65601	AbR65601 Human sec
11	3502	100.0	678	6 ABU99541	Abu99541 Human sec
12	3502	100.0	678	6 ABU58012	Abu58012 Human PRO
13	3502	100.0	678	6 ABU59090	Abu59090 Novel hum
14	3502	100.0	678	6 ABU82602	Abu82602 Human PRO
15	3502	100.0	678	6 ABU82780	Abu82780 Human PRO
16	3502	100.0	678	6 ABU89901	Abu89901 Novel hum
17	3502	100.0	678	6 ABR68150	AbR68150 Human sec
18	3502	100.0	678	6 ABU60521	Abu60521 Human sec
19	3502	100.0	678	6 ABU96203	Abu96203 Novel hum
20	3502	100.0	678	6 ABU92634	Abu92634 Human sec
21	3502	100.0	678	6 ABO08711	ABO08711 Human sec
22	3502	100.0	678	6 ABO02763	ABO02763 Human sec
23	3502	100.0	678	6 ABR74917	AbR74917 Human sec
24	3502	100.0	678	6 ABR94679	AbR94679 Human PRO
25	3502	100.0	678	6 ABU13903	Abu13903 Human PRO

26	3502	100.0	678	6 ABU85652	Abu85652 Human PRO
27	3502	100.0	678	6 ABU98812	Abu98812 Novel hum
28	3502	100.0	678	6 ABU98027	Abu98027 Novel hum
29	3502	100.0	678	6 ABU91733	Abu91733 Novel hum
30	3502	100.0	678	6 ABU89426	Abu89426 Human PRO
31	3502	100.0	678	6 ABU86267	Abu86267 Human sec
32	3502	100.0	678	6 ABU67480	Abu67480 Human sec
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34	3502	100.0	678	6 ABU72488	Abu72488 Novel hum
35	3502	100.0	678	6 ABU90892	Abu90892 Novel hum
36	3502	100.0	678	6 ABO33951	ABO33951 Human sec
37	3502	100.0	678	6 ABR99426	AbR99426 Human sec
38	3502	100.0	678	6 ABR98816	AbR98816 Human sec
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40	3502	100.0	678	6 ABR92239	ABR92239 Human sec
41	3502	100.0	678	6 ABO18880	ABO18880 Human sec
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44	3502	100.0	678	6 ABU85037	Abu85037 Novel hum
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ALIGNMENTS

RESULT 1
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ID AAY66674 standard; protein; 678 AA.
XX
AC AAY66674;
XX
DT 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1277.
XX
KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW Pharmaceutical; receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX
PN W09963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US012252.
XX
PR 02-JUN-1998; 98US-0087607P.
PR 02-JUN-1998; 98US-0087609P.
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PR 03-JUN-1998; 98US-0087827P.
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PR 07-JUL-1998; 98US-0091982P.
PR 09-JUL-1998; 98US-0092182P.
PR 09-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
PR 30-JUL-1998; 98US-0094651P.
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PR 04-AUG-1998; 98US-0095301P.
PR 04-AUG-1998; 98US-0095302P.
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PR 10-AUG-1998; 98US-0095916P.

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PR 31-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 98US-0115565P.
XX
XX (GETH) GENENTECH INC.

PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;

PI Wood WI, Yuan J;

XX WPI; 2000-072883/06.

DR N-PSDB; AA265009.

XX Membrane-bound proteins and related nucleotide sequences.

XX Claim 12; Fig 113; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques

XX Sequence 678 AA;

Query Match 100.0%; Score 3502; DB 3; Length 678;

Best Local Similarity 100.0%; Pred. No. 8.4e-307;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTMRKASVIEFLVLLVTGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPSFIV 60

DB 1 MRTVLTMRKASVIEFLVLLVTGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPSFIV 60

QY 61 KCPAGCQDPKHYHYVGTDTYASYSVCGAAVHSGLVDSGGKILVRKVAGQSGYKGSYNG 120
DB 61 KCPAGCQDPKHYHYVGTDTYASYSVCGAAVHSGLVDSGGKILVRKVAGQSGYKGSYNG 120
QY 121 VQSLSPRWRESFIVLESKPKGKGYTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
DB 121 VQSLSPRWRESFIVLESKPKGKGYTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLATVAVATPTTLPRPSPASATTSIPRQSVGHSQEMDLWSTATTYSQNR 240
DB 181 PVTLMQLLATVAVATPTTLPRPSPASATTSIPRQSVGHSQEMDLWSTATTYSQNR 240
QY 241 PRADPGIQRQDPSGAAPKQPGVADVSGLVPEKBLSTQSLPVSGLDPNCKIDLSFLIDG 300
DB 241 PRADPGIQRQDPSGAAPKQPGVADVSGLVPEKBLSTQSLPVSGLDPNCKIDLSFLIDG 300
QY 301 STSIGKERPRIKQLLADVAQALDIDGAPGLMGVQYQGNPAPATHFNKLTHTNSRDLKTAI 360
DB 301 STSIGKERPRIKQLLADVAQALDIDGAPGLMGVQYQGNPAPATHFNKLTHTNSRDLKTAI 360
QY 361 EKITQRGGLNVGRALISFVTKNPFPSKANGRSKAPNVVVWVDCWPTDKVEEASRLARES 420
DB 361 EKITQRGGLNVGRALISFVTKNPFPSKANGRSKAPNVVVWVDCWPTDKVEEASRLARES 420
QY 421 GINIFPITIEGAENKQYVVEPNFANKAVCRNTGFGYSLHVQSWFGLHKLTLQPLVKRVCD 480
DB 421 GINIFPITIEGAENKQYVVEPNFANKAVCRNTGFGYSLHVQSWFGLHKLTLQPLVKRVCD 480
QY 481 TDLRACSKTCLNSADIGFVINDGSSVGTGNFRTVLQFVTNLTKPEFISDTRIGAVQYT 540
DB 481 TDLRACSKTCLNSADIGFVINDGSSVGTGNFRTVLQFVTNLTKPEFISDTRIGAVQYT 540
QY 541 YEORLEFGPKYSSKPDILNAIKRVGWYSGTSTGAINEFALEOLFVKSPNKKRLMILI 600
DB 541 YEORLEFGPKYSSKPDILNAIKRVGWYSGTSTGAINEFALEOLFVKSPNKKRLMILI 600
QY 601 TDCRSYDDVRIPAWAHLKGVITTYAIGVAAQAQEELEVIATHPARDHSFFVDFDNLHQY 660
DB 601 TDCRSYDDVRIPAWAHLKGVITTYAIGVAAQAQEELEVIATHPARDHSFFVDFDNLHQY 660
QY 661 VPRIIQUICTEFNSQPN 678
DB 661 VPRIIQUICTEFNSQPN 678

RESULT 2

AAU29098 standard; protein; 678 AA.

AC AAU29098;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human PRO polypeptide sequence #75.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX
OS Homo sapiens.
XX
PN W0200168848-A2.
XX
PD 20-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUN-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.
XX (GETH) GENENTECH INC.
FA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
PI WPI; 2001-602746/68.
XX N-PSDB; AAS45999.
PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.
XX Claim 11; Fig 150; 774pp; English.
PS Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
XX The PRO polypeptides and their associated nucleic acids can be used to
CC detect the presence of a tumour in a mammal by comparing the level of
CC expression of a PRO polypeptide in a test sample of cells from the animal
CC and a control sample of normal cells, whereby a higher level of
CC expression in the test sample indicates the presence of a tumour in the
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
CC and rabbits but are preferably human. The polypeptides can be used to
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
CC when contacted with it. A specific polypeptide can be used to stimulate
CC the proliferation or differentiation of chondrocyte cells. The PRO
CC proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders
XX
SQ Sequence 678 AA;

Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTLVTLMKASVTEMFLVLLVTGVSNSKETAKIKRPPKPTVPQINCVDVAGKLIIDPEFTV 60
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Db 61 KCPAGCQDPKHYVYGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
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QY 541 YEORLEFGFDKYSKPKDILNAIKRVGYSWGGTSTGAAINPALEQLFKSKPKNKKLMILI 600
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Db 601 TDCRSYDDVRIIPAAHAKGVITTAIGVAAQAQEELEVIATHPARDHSPFVDFDNLHQY 660
QY 661 VPRIQNICTEFNSQPRN 678
Db 661 VPRIQNICTEFNSQPRN 678

RESULT 3
AAB87542
ID AAB87542 standard; protein; 678 AA.
XX
AC AAB87542;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1277.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.
XX
PR 01-SEP-1999; 99WO-US020111.
XX
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
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PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX
PA (GETH ) GENENTECH INC.
XX
XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX
XX WPI: 2001-183260/18.
DR N-PSDB; AAF92074.
XX
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX
PS Claim 12; Fig 34; 278pp; English.
XX
XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX
SQ Sequence 678 AA;
Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRTLVTLMKASVTEMFLVLLVTGVSNSKETAKIKRPPKPTVPQINCVDVAGKLIIDPEFTV 60
Db 1 MRTLVTLMKASVTEMFLVLLVTGVSNSKETAKIKRPPKPTVPQINCVDVAGKLIIDPEFTV 60
QY 61 KCPAGCQDPKHYVYGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
Db 61 KCPAGCQDPKHYVYGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGSGYKGSYSNG 120
QY 121 VQSLSLPRWRRESFIVLESKPKGVTTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKGVTTPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSQEMDLNSTATTYSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSQEMDLNSTATTYSQNR 240
QY 241 PRADPGIQRODPSGAAPQKPVGADVSLGLVPKEELSTQSLPVS LGDPNCKIDLSELDG 300
Db 241 PRADPGIQRODPSGAAPQKPVGADVSLGLVPKEELSTQSLPVS LGDPNCKIDLSELDG 300
QY 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVYQVGNPATHFNLTHTNSRDLKTAI 360
Db 301 STSIGKRRFRIOQLLADVAQALDIPAGPLMGVYQVGNPATHFNLTHTNSRDLKTAI 360
QY 361 EKITQRGGLSNVGRALISFVTKNPFSSKANGRSNRSAPNVMVDMGWPDKVEASRLARES 420
Db 361 EKITQRGGLSNVGRALISFVTKNPFSSKANGRSNRSAPNVMVDMGWPDKVEASRLARES 420
QY 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRVC 480
Db 421 GINIFITIEGAENKQYVVEPNFANKAVCRITNGFVSLHVQSWFGLHKTLOPLVKRVC 480
```

QY 481 TDLRACSTKCLNSADIGFVIDSSVGTGNTFRVTLQFVNTLTKBEFISDTRIGAVQYT 540
 Db 481 TDLRACSTKCLNSADIGFVIDSSVGTGNTFRVTLQFVNTLTKBEFISDTRIGAVQYT 540
 QY 541 YEORLEFGDFKYSSKPDILNAIKRVGYMSGTSTGAALNPALEQLFKKSKPKKRLMILI 600
 Db 541 YEORLEFGDFKYSSKPDILNAIKRVGYMSGTSTGAALNPALEQLFKKSKPKKRLMILI 600
 QY 601 TGRSYDDVRIPAMAHLKGVTITVAIGVAMAAQBELEVIATHPHARDHSFFVDFDNLHQY 660
 Db 601 TGRSYDDVRIPAMAHLKGVTITVAIGVAMAAQBELEVIATHPHARDHSFFVDFDNLHQY 660
 QY 661 VPRIIONICTEFNSOPRN 678
 Db 661 VPRIIONICTEFNSOPRN 678

RESULT 4
 AAB65197
 ID AAB65197 standard; protein; 678 AA.
 XX AC AAB65197;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1277 (UNQ647) protein sequence SEQ ID NO:179.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
 KW cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US008439.
 XX
 PR 02-JUN-1999; 99WO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 28-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149396P.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy WA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI; 2001-032160/04.

DR N-PSDB; AAF44155.
 XX PRO polynucleotides used to produce polypeptides used to target bioactive
 PT molecules such as toxins, radiolabels or antibodies, to specific cells,
 PT to cause targeted cell death.
 XX
 PS Claim 12; Fig 113; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
 CC be used for targeted delivery of bioactive molecules, such as toxins,
 CC radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
 CC DNA. They may also be used to produce transgenic animals which are used
 CC to develop and screen therapeutically useful reagents. The PRO nucleotide
 CC and protein sequence can be used for tissue typing and in treating
 CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
 CC AAF44470 represent PCR primers and hybridisation probes used in the
 CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
 CC AAB65300 represent human PRO polynucleotide and protein sequences given
 CC in the exemplification of the present invention
 XX
 SQ Sequence 678 AA;

Query Match 100.0%; Score 3502; DB 4; Length 678;
 Best Local Similarity 100.0%; Pred. No. 8.4e-307;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTLVTWKASVIEMLVLLVTVGHSNKEAKIKRPKFTVPQINCDCVAGKIIIDPEFIV 60
 Db 1 MRTLVTWKASVIEMLVLLVTVGHSNKEAKIKRPKFTVPQINCDCVAGKIIIDPEFIV 60
 QY 61 KCPAGCQDPKTHVYGTVDVYASVSCGAAVHSGVLDNSGGKILVRKVGQSGYKSYNG 120
 Db 61 KCPAGCQDPKTHVYGTVDVYASVSCGAAVHSGVLDNSGGKILVRKVGQSGYKSYNG 120
 QY 121 VQSLSLPRWRESFIVLSKPKKGVTPYSALTYSSSKSPAAAGETTKAYQRPPIGTTAQ 180
 Db 121 VQSLSLPRWRESFIVLSKPKKGVTPYSALTYSSSKSPAAAGETTKAYQRPPIGTTAQ 180
 QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASTTSIPRQSVGHRSQBMDLWSTATTYSSQNR 240
 Db 181 PVTLMQLLAVTVAVATPTTLPRPSPAASTTSIPRQSVGHRSQBMDLWSTATTYSSQNR 240
 QY 241 PRADPGIQRQDPSCGAFQKPVGADVSLGLVPKBEISTQSLFVSLGDPNCKIDLSFLIDG 300
 Db 241 PRADPGIQRQDPSCGAFQKPVGADVSLGLVPKBEISTQSLFVSLGDPNCKIDLSFLIDG 300
 QY 301 STSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVVGQDNPATFNLTHTNSRDLKTAI 360
 Db 301 STSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVVGQDNPATFNLTHTNSRDLKTAI 360
 QY 361 EKITQRGSLNVRGAIISFVTKNPFESKANGNRSGAPNVVVVMDGWPDKVBEASRLARES 420
 Db 361 EKITQRGSLNVRGAIISFVTKNPFESKANGNRSGAPNVVVVMDGWPDKVBEASRLARES 420
 QY 421 GINIFFITIEGAENKQYVVEPNFANKAVCRTNGFTYSLHVQSWFGLHKTQLPLVKRVC 480
 Db 421 GINIFFITIEGAENKQYVVEPNFANKAVCRTNGFTYSLHVQSWFGLHKTQLPLVKRVC 480
 QY 481 TDLRACSTKCLNSADIGFVIDSSVGTGNTFRVTLQFVNTLTKBEFISDTRIGAVQYT 540
 Db 481 TDLRACSTKCLNSADIGFVIDSSVGTGNTFRVTLQFVNTLTKBEFISDTRIGAVQYT 540
 QY 541 YEORLEFGDFKYSSKPDILNAIKRVGYMSGTSTGAALNPALEQLFKKSKPKKRLMILI 600
 Db 541 YEORLEFGDFKYSSKPDILNAIKRVGYMSGTSTGAALNPALEQLFKKSKPKKRLMILI 600
 QY 601 TGRSYDDVRIPAMAHLKGVTITVAIGVAMAAQBELEVIATHPHARDHSFFVDFDNLHQY 660
 Db 601 TGRSYDDVRIPAMAHLKGVTITVAIGVAMAAQBELEVIATHPHARDHSFFVDFDNLHQY 660

QY 661 VPRIIQUICTEFSQPRN 678
Db 661 VPRIIQUICTEFSQPRN 678
RESULT 5
ID ABG95867 standard; protein; 678 AA.
AC ABG95867;
DT 10-DEC-2002 (first entry)
XX Human secreted/transmembrane protein PRO1277.
XX Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX Homo sapiens.
XX US2002119130-A1.
XX 29-AUG-2002.
XX 06-DEC-2001; 2001US-00006867.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 22-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085759P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089653P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 26-JUN-1998; 98US-0090696P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096757P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096959P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099812P.
PR 16-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101293P.
PR 23-SEP-1998; 98US-0101475P.

PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.
PR 24-SEP-1998; 98US-0101916P.
PR 30-SEP-1998; 98US-0102570P.
PR 06-OCT-1998; 98US-0103449P.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021194.
PR 22-DEC-1999; 99WO-US030720.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032378.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX

(GETH) GENENTECH INC.

Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

WPI; 2002-731348/79.
N-PSDB; ABS74394.

New isolated secreted and transmembrane PRO polypeptide useful for
modulating biological activity of a cell, or for treating sports-related
joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 34; 399pp; English.

The invention relates to an isolated secreted and transmembrane PRO
polypeptide having 80 % sequence identity to a sequence appearing as
ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
extracellular domain of the proteins with their associated signal peptide
or lacking its associated signal peptide. Also included are the nucleic
acids encoding the proteins, vectors, host cells, fusion proteins and
antibodies which specifically bind to the proteins. The proteins are
useful for detecting a polypeptide designated as A, B, C or D in a sample
suspected of containing an A, B, C or D polypeptide, by contacting the
sample with a polypeptide designated as E, F, G, H or I (or vice versa)
and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
conjugate in the sample, where the formation of the conjugate is
indicative of the presence of an A, B, C or D polypeptide in the sample.
where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
H or I polypeptide is labeled with a detectable label or is attached to a
solid support. The proteins are useful for linking a bioactive molecule
to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
or I, or antibodies against them are useful for modulating a biological
activity of a cell expressing a polypeptide designated as A, B, C or D or
E, F, G, H, or I. The cell is killed. The proteins are useful for
identifying agonists or antagonists, for the preparation of a medicament

CC useful in the treatment of a condition which is responsive to the
CC proteins, as molecular weight markers for protein electrophoresis
CC purposes, and as therapeutic agents for treating sports-related joint
CC problems, articular cartilage defects, osteoarthritis or rheumatoid
CC arthritis. Nucleic acids encoding the proteins are useful as
CC hybridisation probes, in chromosome and gene mapping, in the generation
CC of anti-sense RNA and DNA, for the preparation of the proteins, to
CC generate transgenic or knockout animals which are useful in the
CC development and screening of therapeutic useful reagents, for chromosome
CC identification, and in gene therapy. The antibody is useful as a
CC therapeutic agent, in a diagnostic assay and for affinity purification of
CC the protein from recombinant cell culture natural sources. The present
CC sequence represents a novel secreted or transmembrane protein of the
CC invention
XX
SQ Sequence 678 AA;

Query Match 100.0%; Score 3502; DB 5; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTLVTWKASVIEMLFVLLVTGVHSHKETAKKIKRPFTVPQINCDVKAGKIIDPEFIV 60
Db 1 MRTLVTWKASVIEMLFVLLVTGVHSHKETAKKIKRPFTVPQINCDVKAGKIIDPEFIV 60
Qy 61 KCPAGCQDPKTHVYGTVDYASVSYCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Db 61 KCPAGCQDPKTHVYGTVDYASVSYCGAAVHSGVLDNSGGKILVRKVGQSGYKGSYNG 120
Qy 121 VQSLSLRWRRESFVLESKPKKGGVTPSALTYSSSKSPAAOAGETTKAYQRPPIGTTAQ 180
Db 121 VQSLSLRWRRESFVLESKPKKGGVTPSALTYSSSKSPAAOAGETTKAYQRPPIGTTAQ 180
Qy 181 PVTLMQLLAVTVATPTTLPRPSPAASTTSIPRQSVGHRSGMDLWSTATTYSSQNR 240
Db 181 PVTLMQLLAVTVATPTTLPRPSPAASTTSIPRQSVGHRSGMDLWSTATTYSSQNR 240
Qy 241 PRADPGIQRQDPGSAAPQKPGVADVSLGVPKEBELSTQSLPVSGLDPNCKIDLSFLIDG 300
Db 241 PRADPGIQRQDPGSAAPQKPGVADVSLGVPKEBELSTQSLPVSGLDPNCKIDLSFLIDG 300
Qy 301 STSICKRRPRIQKOLLADVAQALDIGPAGPLMGVYQYGDNPATHPNLKTHNRSRLKTAI 360
Db 301 STSICKRRPRIQKOLLADVAQALDIGPAGPLMGVYQYGDNPATHPNLKTHNRSRLKTAI 360
Qy 361 EKITQRGSLSNVGRASIFVTNFKNSKANGNSGAPNVMVDGMPDTKVBEASRLARES 420
Db 361 EKITQRGSLSNVGRASIFVTNFKNSKANGNSGAPNVMVDGMPDTKVBEASRLARES 420
Qy 421 GINIFFITIEGAENEKQYVVEPNPANKAVCKRTNGFYSLRVQSWFGLHKTQLPLVKRVD 480
Db 421 GINIFFITIEGAENEKQYVVEPNPANKAVCKRTNGFYSLRVQSWFGLHKTQLPLVKRVD 480
Qy 481 TDLRACSTKCLNSADIGFVDDSSSVGNGFRTVLQFVTNLTKEPEISDTDTTRIGAVOYT 540
Db 481 TDLRACSTKCLNSADIGFVDDSSSVGNGFRTVLQFVTNLTKEPEISDTDTTRIGAVOYT 540
Qy 541 YEQRLEFGDFKYSSKPDILNAIKRVGYWSGGTSTGAAINPFALEBQLFKSKNKRKLMILI 600
Db 541 YEQRLEFGDFKYSSKPDILNAIKRVGYWSGGTSTGAAINPFALEBQLFKSKNKRKLMILI 600
Qy 601 TDGRSYDDVRIPAMAHLKGVITTAIGVAMAQEELEVIATHPARDHSPFVDFDNLHGY 660
Db 601 TDGRSYDDVRIPAMAHLKGVITTAIGVAMAQEELEVIATHPARDHSPFVDFDNLHGY 660
Qy 661 VPIIIONICTEFNSQPRN 678
Db 661 VPIIIONICTEFNSQPRN 678

RESULT 6
ABU58474
ID ABU58474 standard; protein; 678 AA.

XX AC ABU58474;
XX DT 15-APR-2003 (first entry)
XX DE Human PRO polypeptide #75.
XX KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
XX KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
XX KW antibody-dependent enzyme mediated prodrug therapy.
XX OS Homo sapiens.
XX PN US2003027272-A1.
XX PD 06-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176492.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 18-SEP-1997; 97US-0059266P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 21-OCT-1997; 97US-0063486P.
XX PR 24-OCT-1997; 97US-0063120P.
XX PR 24-OCT-1997; 97US-0063121P.
XX PR 28-OCT-1997; 97US-0063540P.
XX PR 28-OCT-1997; 97US-0063541P.
XX PR 28-OCT-1997; 97US-0063544P.
XX PR 28-OCT-1997; 97US-0063564P.
XX PR 29-OCT-1997; 97US-0063734P.
XX PR 31-OCT-1997; 97US-0063870P.
XX PR 31-OCT-1997; 97US-0064103P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 21-NOV-1997; 97US-0066120P.
XX PR 24-NOV-1997; 97US-0066466P.
XX PR 11-DEC-1997; 97US-0069335P.
XX PR 12-DEC-1997; 97US-0069425P.
XX PR 17-DEC-1997; 97US-0069870P.
XX PR 18-DEC-1997; 97US-0068017P.
XX PR 10-MAR-1998; 98US-0077450P.
XX PR 11-MAR-1998; 98US-0077632P.
XX PR 11-MAR-1998; 98US-0077649P.
XX PR 20-MAR-1998; 98US-0078866P.
XX PR 20-MAR-1998; 98US-0078939P.
XX PR 27-MAR-1998; 98US-0079664P.
XX PR 27-MAR-1998; 98US-0079786P.
XX PR 31-MAR-1998; 98US-0080107P.
XX PR 31-MAR-1998; 98US-0080194P.
XX PR 01-APR-1998; 98US-0080327P.
XX PR 08-APR-1998; 98US-0081049P.
XX PR 08-APR-1998; 98US-0081070P.
XX PR 09-APR-1998; 98US-0081195P.
XX PR 15-APR-1998; 98US-0081838P.
XX PR 21-APR-1998; 98US-0082568P.
XX PR 21-APR-1998; 98US-0082569P.
XX PR 22-APR-1998; 98US-0082704P.
XX PR 22-APR-1998; 98US-0082797P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 29-APR-1998; 98US-0083495P.
XX PR 29-APR-1998; 98US-0083496P.
XX PR 29-APR-1998; 98US-0083499P.
XX PR 29-APR-1998; 98US-0083559P.
XX PR 05-MAY-1998; 98US-0084366P.
XX PR 06-MAY-1998; 98US-0084414P.
XX PR 07-MAY-1998; 98US-0084633P.
XX PR 07-MAY-1998; 98US-0084640P.
XX PR 15-MAY-1998; 98US-0084643P.
XX PR 15-MAY-1998; 98US-0085579P.
XX PR 15-MAY-1998; 98US-0085580P.
XX PR 15-MAY-1998; 98US-0085582P.
XX PR 15-MAY-1998; 98US-0085700P.

PR	18-MAY-1998;	98US-00860233P.	PR	18-AUG-1998;	98US-0096949P.
PR	22-MAY-1998;	98US-00863392P.	PR	18-AUG-1998;	98US-00969559P.
PR	22-MAY-1998;	98US-0086486P.	PR	18-AUG-1998;	98US-0097022P.
PR	26-MAY-1998;	98US-0087098P.	PR	26-AUG-1998;	98US-0097952P.
PR	28-MAY-1998;	98US-0087208P.	PR	26-AUG-1998;	98US-0097954P.
PR	02-JUN-1998;	98US-0087609P.	PR	26-AUG-1998;	98US-0097955P.
PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087877P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088025P.	PR	26-AUG-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098716P.
PR	04-JUN-1998;	98US-0088029P.	PR	02-SEP-1998;	98US-0098803P.
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XX AC ABU88022;
XX DT 07-JUL-2003 (first entry)
XX DE Novel human secreted and transmembrane protein PRO1277.
XX KW Human; secreted and transmembrane protein; PRO; gene therapy;
KW tumour necrosis factor-alpha release; TNF-alpha release;
KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
KW prostate tumour; rectal tumour; cervical tumour; liver tumour.
XX OS Homo sapiens.
XX PN US2003032127-A1.
XX PD 13-FEB-2003.
XX PF 26-JUN-2002; 2002US-00183012.
XX PR 18-SEP-1997; 97US-0059263P.
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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 VQSLSLPRWRRESFIVLESKPKKGVTPYSALTYSSSSPAAQAGETTAKAYORPPIPGTTAQ 180
Db 121 VQSLSLPRWRRESFIVLESKPKKGVTPYSALTYSSSSPAAQAGETTAKAYORPPIPGTTAQ 180

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Qy 241 PRADPGIQRQDPGSAAPQKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDG 300
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Db 661 VPRIIQNICTEPNSQPRN 678

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ID ABU84337 standard; protein; 678 AA.
XX AC ABU84337;
XX DT 02-AUG-2003 (first entry)
XX DE Human secreted/transmembrane protein (PRO) #75.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX OS Homo sapiens.
XX PN US2003032112-A1.
XX PD 13-FEB-2003.
XX PF 21-JUN-2002; 2002US-00176756.
XX 18-SEP-1997; 97US-0059263P.
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Qy	121	VQSLSPRWRESFVLESKPKGVTYPSALTYSSKSPAAAGETTKAYQRPPIPGTTAQ	180
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Qy	181	PVTLMQLLAVTAVATPTTLPRPSPAATTSIPRQSVGHRSQEMDLWSTATYTSSQNR	240
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Dd	61	KCPAGCQDPKYHVYGTDDYVASYSYCGBAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
Qy	121	VQSLSLPRWRESPIVLESKPKGVTPSALTYSSSKSPAAQGETTKAYORPPIPGTTAQ 180
Dd	121	VQSLSLPRWRESPIVLESKPKGVTPSALTYSSSKSPAAQGETTKAYORPPIPGTTAQ 180
Qy	181	PVTLMOLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSQSMDLNSTATTYTSSQNR 240
Dd	181	PVTLMOLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHRSQSMDLNSTATTYTSSQNR 240
Qy	241	PRADPGIORQDPSGAAPQKPCADVSLGLVPKEELSTQSLBPVS LGDPNCKIDL SFLIDG 300
Dd	241	PRADPGIORQDPSGAAPQKPCADVSLGLVPKEELSTQSLBPVS LGDPNCKIDL SFLIDG 300
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Dd	481	TDRLACSTKLNSADIGFVIDGSSSVGTGNFTVLQFVTNLTKBFEISDTDFRICAQVQT 540
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Dd	541	YEORLEFGFDKYSSKPDIIINALIKRYGYSGGSTGTCAAINFALBQLPFKSKPNKRKLMILI 600
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Dd	601	TGERSYDDVRIPAMAHLKGVIITYAIGVAWAQQEELVIATHPARDHSPFVDFONLHQY 660
Qy	661	VPRIIONICTBFNSQPRN 678
Dd	661	VPRIIONICTBFNSQPRN 678

RESULT 10

ABR65601	
ID	ABR65601 standard; protein; 678 AA.
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AC	ABR65601;
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DT	05-AUG-2003 (first entry)
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DE	Human secreted polypeptide PRO1277, SEQ ID NO:150.
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KW	Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnery; gene therapy.
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OS	Homo sapiens.
XX	
PN	US2003036159-A1.
XX	
PD	20-FEB-2003.
XX	
PP	02-JUL-2002; 2002US-00188773.
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Qy	121	121	121
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Qy	481	TDLRACSKTCLNSADIGFVIGDSSSVGTGNPRTVLQFVTLTKFEFISDTRIGAVQYT	540	PR	08-APR-1998;	98US-0081049P.
				PR	08-APR-1998;	98US-0081049P.
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				PR	09-APR-1998;	98US-0081195P.
Qy	541	YEQRLEFGDKYSSKPDILNAIKRVGYWSGTTSTGAAINPALEQLFKKSPNKKKLMILI	600	PR	15-APR-1998;	98US-0081838P.
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RESULT 11

ABU99541
ID ABU99541 standard; protein; 678 AA.
XX AC ABU99541;
XX DT (first entry)
XX DE Human secreted/transmembrane protein (PRO) #75.
XX KW Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW tissue typing.
XX OS Homo sapiens.
XX PN US2003040070-A1.
XX PD 27-FEB-2003.
XX PF 27-JUN-2002; 2002US-00184627.
XX PR 18-SEP-1997; 97US-0059263P.
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PR 06-OCT-1998; 98US-0103449P;
PR 07-OCT-1998; 98US-00168978;

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Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KCPAGCQDPKHVYGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
QY 121 VQSLSLPRWRESFVLESKPKKGVTPYPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VQSLSLPRWRESFVLESKPKKGVTPYPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ 180
QY 181 PVTLMOLLAVTVAVATPTTLPRPSPSAATSTSIIPRQSVGHSQEMDLKSTATYTSSQNR 240
DB 181 PVTLMOLLAVTVAVATPTTLPRPSPSAATSTSIIPRQSVGHSQEMDLKSTATYTSSQNR 240
QY 241 PRADPGIORQDPGSAPOKPGADVSLGLVPKBEISTOSLEPVSLGDPNCKIDLSPIDG 300
DB 241 PRADPGIORQDPGSAPOKPGADVSLGLVPKBEISTOSLEPVSLGDPNCKIDLSPIDG 300
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DB 301 STSIGKRFRFRIQKOLLADVAQALDIPAGPLMGVVQYGDNPATHPNLKTHTNSRDLKTAI 360
QY 361 EKITORGGLSNVGRASIVTNTKPFKANGNSGAPNVVVWVDCGPTDKVEASRLARES 420
DB 361 EKITORGGLSNVGRASIVTNTKPFKANGNSGAPNVVVWVDCGPTDKVEASRLARES 420
QY 421 GINIFFITIEGAENEKQYVVEPNPANKAVCTNGTFYSLHVQSWFGLHKTLOPLVKRVC 480
DB 421 GINIFFITIEGAENEKQYVVEPNPANKAVCTNGTFYSLHVQSWFGLHKTLOPLVKRVC 480
QY 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTLTKBEISDTRIGAVQYT 540
DB 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTLTKBEISDTRIGAVQYT 540
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DB 601 TDGRSYDDVRIPMAAHLKGVTITTAIGVAAQAQBELEVIATHPARDHSFPVDFDNLHOY 660
QY 661 VPRIIONICTEFPNSQPRN 678
DB 661 VPRIIONICTEFPNSQPRN 678
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AC ABUS8012;
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DT 14-APR-2003 (first entry)
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DE Human PRO polypeptide #44.
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KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADAPT;
KW antibody-dependent enzyme mediated prodrug therapy.
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OS Homo sapiens.
XX
PN US2003027163-A1.
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PD 06-FEB-2003.
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PP 15-NOV-2001; 2001US-00997666.
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Query Match 100.0%; Score 3502; DB 6; Length 678;		
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Qy	121	VQSLSLPRWRSFVILESKPKKGVTPPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
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Query Match

Best Local Similarity

Matches

100.0%;

100.0%;

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Score

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DB

6;

Length

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XX 27-JUN-2003 (first entry)
XX Human PRO polypeptide #75.
XX Human; PRO polypeptide; secreted and transmembrane protein; tumour;
XX Chromosome mapping; gene mapping; cytostatic.
XX Homo sapiens.
XX US2003032113-A1.
XX 13-FEB-2003.
XX 20-JUN-2002; 2002US-00176911.
PR 18-SEP-1997; 97US-0059263P.
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PR	24-JUL-1998;	98US-0094006P.	Db	61		120
PR	04-AUG-1998;	98US-0095282P.	Qy	121	VQSLSLPRWRESFIVLESKPKGVYTPSALTYSSSKSPAAQAGETTKAYORPPIPGTTAQ	180
PR	10-AUG-1998;	98US-0095998P.	Db	121		180
PR	10-AUG-1998;	98US-0096012P.	Qy	181	PVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSGEMDLMSTATTSSQNR	240
PR	17-AUG-1998;	98US-0096757P.	Db	181		240
PR	17-AUG-1998;	98US-0096766P.	Qy	241	PRADPGIORODPSGAAPQKQVGVADVSLGVPKBELSTQSLPEVSLGDPNCKIDLSFLIDG	300
PR	17-AUG-1998;	98US-0096867P.	Db	241		300
PR	17-AUG-1998;	98US-0096891P.	Qy	301	STSIGKRFRIOKOLLADVAQALDIGPAGPLGVVQYGDNPATFNKLTHTNSRDLKTAI	360
PR	17-AUG-1998;	98US-0096949P.	Db	301		360
PR	18-AUG-1998;	98US-0096959P.	Qy	361	EKITQRGGLSNVGRASIFVTNFPFSKANGNRSGAPNVVVVWDGMPDKVEEASRLAES	420
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PR	26-AUG-1998;	98US-0097952P.	Qy	421	GINIFPTTIEGAAENKQYVVEPNFANKAVCRINGFYSLVHVSQWFGHLHKTLOPLVKRCD	480
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PR	26-AUG-1998;	98US-0097971P.	Qy	481	TDRLACSKTCLNSADIGFVIDGSSSVGCTGNFRTVLQFVTNLTKFEFISDTRIGAVQYT	540
PR	26-AUG-1998;	98US-0097974P.	Db	481		540
PR	26-AUG-1998;	98US-0098014P.	Qy	541	YEORLEPGDKYSSKPDILNAIKRVGVWSGGTSTGAAINFALBOLFKKSKPNKRLMILI	600
PR	01-SEP-1998;	98US-0098716P.	Db	541		600
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PR	02-SEP-1998;	98US-0098843P.	Db	661		
PR	09-SEP-1998;	98US-0099602P.			VPRIIQNICTEFNSQPRN 678	
PR	10-SEP-1998;	98US-0099741P.				
PR	10-SEP-1998;	98US-0099754P.				
PR	10-SEP-1998;	98US-0099763P.				
PR	10-SEP-1998;	98US-0099812P.				
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PR	17-SEP-1998;	98US-0100684P.				
PR	17-SEP-1998;	98US-0100919P.				
PR	17-SEP-1998;	98US-0100930P.				
PR	18-SEP-1998;	98US-0100849P.				
PR	18-SEP-1998;	98US-0101014P.				
PR	18-SEP-1998;	98US-0101068P.				
PR	23-SEP-1998;	98US-0101471P.				
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PR	23-SEP-1998;	98US-0101475P.				
PR	23-SEP-1998;	98US-0101738P.				
PR	24-SEP-1998;	98US-0101739P.				
PR	24-SEP-1998;	98US-0101743P.				
PR	24-SEP-1998;	98US-0101922P.				
PR	25-SEP-1998;	98US-0101786P.				
PR	25-SEP-1998;	98US-0102207P.				
PR	29-SEP-1998;	98US-0102240P.				
PR	29-SEP-1998;	98US-0102330P.				
PR	29-SEP-1998;	98US-0102331P.				
PR	30-SEP-1998;	98US-0102487P.				
PR	30-SEP-1998;	98US-0102570P.				
PR	30-SEP-1998;	98US-0102571P.				
PR	01-OCT-1998;	98US-0102684P.				
PR	01-OCT-1998;	98US-0102687P.				
PR	02-OCT-1998;	98US-0102965P.				
PR	06-OCT-1998;	98US-0103258P.				
PR	06-OCT-1998;	98US-0103449P.				
PR	07-OCT-1998;	98US-00168978.				
PR	07-OCT-1998;	98US-0103395P.				

Search completed: May 27, 2004, 16:45:59
Job time : 63 secs

Query Match 100.0%; Score 3502; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 8.4e-307;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MRTVLTWKASVTEMFLVLLVTGVHNSKETAKIKRPFVTPQINCVDKAGKIIDPEFIV 60
Db 1 MRTVLTWKASVTEMFLVLLVTGVHNSKETAKIKRPFVTPQINCVDKAGKIIDPEFIV 60

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:42:38 ; Search time 51 Seconds
(without alignments)
4194.536 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502

Sequence: 1 MRTLVTWKASVIEMLVLL.....QVPRRIIICTEFNSQPRN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3502	100.0	678	4	Q9UDN0	Q9udn0 homo sapien
2	3484.5	99.5	693	4	Q96DM8	Q96dm8 homo sapien
3	3344	95.5	656	4	Q96DT1	Q96dt1 homo sapien
4	2823	80.6	650	11	Q8VH15	Q8vhi5 mus musculu
5	2818	80.5	652	6	Q95LI2	Q95li2 bos taurus
6	2801	80.0	650	11	Q8K047	Q8k047 mus musculu
7	2796	79.8	650	11	Q9CY21	Q9cy21 mus musculu
8	2682	76.6	628	11	Q8BQ41	Q8bq41 mus musculu
9	1187.5	33.9	553	13	Q8AW56	Q8aw56 brachydanio
10	1017.5	29.1	494	4	Q96IU6	Q96iu6 homo sapien
11	512	14.6	490	13	Q7SYT5	Q7sy5 xenopus lae
12	493	14.1	500	11	Q80VN5	Q80vn5 mus musculu
13	485	13.8	507	13	Q7ZVP3	Q7zvp3 brachydanio
14	463	13.2	1182	11	Q8C6K9	Q8c6k9 mus musculu
15	447.5	12.8	540	4	Q8N2M5	Q8n2m5 homo sapien
16	435.5	12.4	1703	11	Q9Z019	Q9z019 mus musculu

17	409	11.7	488	4	Q8N2M7	Q8n2m7 homo sapien
18	378	10.8	2657	11	Q88493	Q88493 mus musculu
19	360	10.3	1016	4	Q8NDE6	Q8nde6 homo sapien
20	357.5	10.2	937	4	Q96FT5	Q96ft5 homo sapien
21	350.5	10.0	1797	11	Q80X19	Q80x19 mus musculu
22	339.5	9.7	956	11	Q99K64	Q99k64 mus musculu
23	337.5	9.6	956	11	Q8R542	Q8r542 mus musculu
24	334	9.5	721	11	Q8CE01	Q8ce01 mus musculu
25	326	9.3	1253	6	Q97566	Q97566 canis famil
26	326	9.3	2936	6	Q7YRK8	Q7yrk8 canis famil
27	324	9.3	2944	11	Q63870	Q63870 mus musculu
28	323	9.2	517	4	Q43853	Q43853 homo sapien
29	314.5	9.0	567	5	Q18048	Q18048 caenorhabdi
30	313	8.9	453	5	Q8T5C2	Q8t5c2 mytilus gal
31	307	8.8	444	5	Q8T5C3	Q8t5c3 mytilus edu
32	300	8.6	441	5	Q8T6U5	Q8t6u5 mytilus edu
33	300	8.6	755	4	Q00261	Q00261 homo sapien
34	298	8.5	537	4	Q96AA0	Q96aa0 homo sapien
35	298	8.5	715	4	Q7Z5X1	Q7z5x1 homo sapien
36	290.5	8.3	954	4	Q8WV8	Q8wv8 homo sapien
37	290.5	8.3	957	4	Q9H0V3	Q9h0v3 homo sapien
38	290.5	8.3	957	4	Q96P44	Q96p44 homo sapien
39	289.5	8.3	1626	4	Q8NFW1	Q8nfw1 homo sapien
40	282.5	8.1	2813	11	Q8C1Z8	Q8c1z8 mus musculu
41	281	8.0	1472	13	Q90ZAO	Q90za0 gallus gall
42	279	8.0	2104	5	Q964N4	Q964n4 caenorhabdi
43	279	8.0	2104	5	Q21281	Q21281 caenorhabdi
44	271.5	7.8	419	6	Q97925	Q97925 macropus gi
45	271	7.7	549	6	Q02808	Q02808 bos taurus

ALIGNMENTS

RESULT 1

ID	Q9UDN0	PRELIMINARY;	PRT;	678 AA.
AC	Q9UDN0;			
DT	01-MAY-2000 (Tremblrel. 13, Created)			
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)			
DE	Similar to Coch-5B2.			
GN	WUGSC:H NH0294L11.1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99063792; PubMed=9847074;			
RA	Suleston J.E., Waterston R.;			
RT	"Toward a complete human genome sequence.";			
RL	Genome Res. 8:1097-1108(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Corde M., Kalicki J., Ames M.;			
RT	"The sequence of Homo sapiens BAC clone Rp11-294L11.";			
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Waterston R.;			
RT	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AC007363; AAP19243.1; --			
DR	HSSP; P11215; 1JLM.			
DR	InterPro; IPR004043; LCCL dom.			
DR	InterPro; IPR002035; VWF_A.			
DR	Pfam; PF03815; LCCL; 1.			
DR	Pfam; PF00092; vwa; 2.			
DR	PRINTS; PR00453; VWFADOMAIN.			
DR	SMART; SM00603; LCCL; 1.			
DR	SMART; SM00327; VWA; 2.			
DR	PROSITE; PS50820; LCCL; 1.			
DR	PROSITE; PS50234; VWA; 2.			

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SQ SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;
Query Match 100.0%; Score 3502; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.3e-242; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

QY 1 MRTVLTMTKASVEMFLVLLVTGVHNSKETAKKIKRPKPTVPOINCVDVKAGKIIDPEPIV 60
DB 1 MRTVLTMTKASVEMFLVLLVTGVHNSKETAKKIKRPKPTVPOINCVDVKAGKIIDPEPIV 60

QY 61 KCPAGCQDPKHYVGTDTVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120
DB 61 KCPAGCQDPKHYVGTDTVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120

QY 121 VOSLSLPRWRRESFVLESPPKGGVTVPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VOSLSLPRWRRESFVLESPPKGGVTVPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240

QY 241 PRADPGIQRDPSGAAPQKPGVADVSLGLVPKEELSTQSLPVPVSLGDPNCKIDLSEFLDG 300
DB 241 PRADPGIQRDPSGAAPQKPGVADVSLGLVPKEELSTQSLPVPVSLGDPNCKIDLSEFLDG 300

QY 301 STSISGRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAI 360
DB 301 STSISGRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAI 360

QY 361 EKITQGGLSNVGRAISFVTKNPFSSKANGRSGAPNVVWVDGWPDKVBEASRLARES 420
DB 361 EKITQGGLSNVGRAISFVTKNPFSSKANGRSGAPNVVWVDGWPDKVBEASRLARES 420

QY 421 GINIPIITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWPGLHKTLOPLKRVCD 480
DB 421 GINIPIITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWPGLHKTLOPLKRVCD 480

QY 481 TDLRACKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLTKFPIISDTDRIGAVQYT 540
DB 481 TDLRACKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLTKFPIISDTDRIGAVQYT 540

QY 541 YEQRLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQLPKSKPNKRKLMILI 600
DB 541 YEQRLEFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQLPKSKPNKRKLMILI 600

QY 601 TDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPARDHSFVDFDNLHQY 660
DB 601 TDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPARDHSFVDFDNLHQY 660

QY 661 VPRIIQNICTEFNQSPRN 678
DB 661 VPRIIQNICTEFNQSPRN 678
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RESULT 2

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Q96DM8 PRELIMINARY; PRT; 693 AA.
AC Q96DM8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ32210.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
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RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Maetuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Negahari K., Masuho Y., Negai K., Isogai T.;
RT "NEO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056772; BAB71279.1; -.
DR Genew; HGNC:12697; VIT.
DR InterPro; IPR004043; LCCL dom.
DR InterPro; IPR002035; WWP_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; WVFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS00820; LCCL; 1.
DR PROSITE; PS02334; WFA; 2.
DR Hypothetical protein.
KW SEQUENCE 693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;
Query Match 99.5%; Score 3484.5; DB 4; Length 693;
Best Local Similarity 97.8%; Pred. No. 2.4e-241; Indels 15; Gaps 1;
Matches 678; Conservative 0; Mismatches 0;

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DB 1 MRTVLTMTKASVEMFLVLLVTGVHNSKETAKKIKRPKPTVPOINCVDVKAGKIIDPEPIV 60

QY 61 KCPAGCQDPKHYVGTDTVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120
DB 61 KCPAGCQDPKHYVGTDTVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120

QY 121 VOSLSLPRWRRESFVLESPPKGGVTVPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180
DB 121 VOSLSLPRWRRESFVLESPPKGGVTVPSALTYSKSPAAQAGETTKAYORPPIPGTTAQ 180

QY 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240
DB 181 PVTLMQLLAVTVAVATPTTLPRPSPAASSTTSIPRQSVGHRSGQEMDLWSTATYTSSQNR 240

QY 241 PRADPGIQRDPSGAAPQKPGVADVSLGLVPKEELSTQSLPVPVSLGDPNCKIDLSEFLDG 285
DB 241 PRADPGIQRDPSGAAPQKPGVADVSLGLVPKEELSTQSLPVPVSLGDPNCKIDLSEFLDG 300

QY 286 GPNCKIDLSFLIDGSTSIGKRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHF 345
DB 286 GPNCKIDLSFLIDGSTSIGKRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHF 360

QY 301 GPNCKIDLSFLIDGSTSIGKRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHF 360
DB 301 GPNCKIDLSFLIDGSTSIGKRRPRIQKOLLADVAQALDIGPAGPLMGVQYGDNPATHF 360

QY 346 NLKHTNSRDLKTAIEKITQGGLSNVGRAISFVTKNPFSSKANGRSGAPNVVWVDGW 405
DB 346 NLKHTNSRDLKTAIEKITQGGLSNVGRAISFVTKNPFSSKANGRSGAPNVVWVDGW 420

QY 406 PTDKVEASRLARESGINIFPITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWP 465
DB 406 PTDKVEASRLARESGINIFPITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWP 480

QY 421 PTDKVEASRLARESGINIFPITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWP 480
DB 421 PTDKVEASRLARESGINIFPITTEGAENKQYVVEPNPANKAVCRNNGFYSLFVQSWP 480

QY 466 GLHKTLOPLKRVCDTDLRACKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLTKFP 525
DB 466 GLHKTLOPLKRVCDTDLRACKTCLNSADIGFVIDGSSVGTGNFRTVLOFVNTLTKFP 540

QY 526 EISDTRIGAVQYTYEQRLERFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQL 585
DB 526 EISDTRIGAVQYTYEQRLERFGDKYSSKPDILNAIKRVGWSGGTSTGAAINPALEQL 600

QY 586 FKSKPNKRKLMILTDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPAR 645
DB 586 FKSKPNKRKLMILTDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPAR 660

QY 601 FKSKPNKRKLMILTDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPAR 660
DB 601 FKSKPNKRKLMILTDCRSYDDVRIIPAMAAHLKGVTIYALGVANAAQSELEVIATHPAR 660

QY 646 DHSFFVDFDNLHQYVPRIIQNICTEFNQSPRN 678
DB 646 DHSFFVDFDNLHQYVPRIIQNICTEFNQSPRN 693
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QY 418 RESGNIPTITIEGAARENEKQVVEPNFANKAVCRITNGFYSLVHVSQSWFGLHKTLOPLVKR 477
DB 390 RESGINVFITVEGAAREKQHVVEPFASKAVCRITNGFYSFNVQSWLSLHKTIVQPLVKR 449
QY 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAV 537
DB 450 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAV 509
QY 538 QYTYEORLEFGDKYSSKPDILNAIKRVGVWMSGTGTGAALNPALEQLFKSKPKNRKLM 597
DB 510 QYTYEORLEFGDKYSSKPDILNAIKRVGVWMSGTGTGAALNPALEQLFKSKPKNRKLM 569
QY 598 ILIITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAEELEVIATHPARDHSFPVDFDNL 657
DB 570 ILIITDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAEELEVIATHPARDHSFPVDFDNL 629
QY 658 HQVPRIIQNICTEFNSQPRN 678
DB 630 YKIAPRIIQNICTEFNSQPRN 650

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RESULT 5

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Q95LI2 PRELIMINARY; PRT; 652 AA.
AC Q95LI2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vitrin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Ren Z.-X., Liu J.G., Mayne R.;
RT "Bovine vitrin cDNA sequence."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF063832; AAL18262.2; -.
DR InterPro; IPR004043; LCCL dom.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 652 AA; 70872 MW; 3512421CA6987C51 CRC64;

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Query Match 80.5%; Score 2818; DB 6; Length 652;
Best Local Similarity 79.8%; Pred. No. 1.5e-193;
Matches 541; Conservative 49; Mismatches 62; Indels 26; Gaps 2;

QY 1 MRTVLTMKASVTEMFLVLLVTGVHNSKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIV 60
DB 1 MGIWPTMKASVTEMFLVLLVTGVHNSKETAKKIKRPKFTVPQISCVDKAGKINVEFIV 60
QY 61 KCPAGCDPKYHYVGTVDVYASVSCGAHVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120
DB 61 KCPGCGDPRHYVGVADVYASVSCGAHVHSGVLDNSGGKILVRKVAGSGYKGSYNG 120
QY 121 VQSLSLPRWRRESFVLVLSKPKGVITYPSALTYSSSKSPAQAAGTTKAYORPPIPGTTAQ 180
DB 121 VQSLSLPRWRRESFVVSSEKPKGVITYPSALTYSSSKSPAQAAGTTKAYORPPIPGTTAQ 180
QY 181 PVTLMQLLATVAVATPTTLPRPSPAASITTSIPRQSVGHSRQEMDLMTATYTSSQNR 240
DB 181 FVTVTQAPGTAIBATHTTLTKPSPSAGSTASGLRQPAGQRSKDL----- 226

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QY 241 PRADPGIORQDPSGAARFQKPGVADVSLGLVPKEELSTQSLPESVSLGDPNCKIDLSFLIDG 300
DB 227 --GEP-----ALWKPESVLLDAGFVPKEELSTQSLPESQDPSCKVDLSFLIDG 274
QY 301 STSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVOYGNPATFNLKHTNDRDLKTAI 360
DB 275 SSSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVOYGNPATFNLKHTNDRDLKTAI 334
QY 361 EKITORGGLSNVGRASISFVTKNPFSSKANGRGAPNVVVMVDGWPTDKVERASRLARES 420
DB 335 EKISORGGLSNVGRASISFVTKNPFSSKANGRGAPNVVVMVDGWPTDKVERASRLARES 394
QY 421 GINIPIPTITIEGAARENEKQVVEPNFANKAVCRITNGFYSLVHVSQSWFGLHKTLOPLVKR 480
DB 395 GYNIPIPTITIEGAARENEKQVVEPNFANKAVCRITNGFYSLVHVSQSWFGLHKTLOPLVKR 454
QY 481 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAVQYT 540
DB 455 TDLRACSKTCLNSADIGFVIDGSSSVGTGNFRITVLOFVFNLTKEFEISDTRIGAVQYT 514
QY 541 YEORLEFGDKYSSKPDILNAIKRVGVWMSGTGTGAALNPALEQLFKSKPKNRKLMILI 600
DB 515 YEORLEFGDKYSSKPDILNAIKRVGVWMSGTGTGAALNPALEQLFKSKPKNRKLMILI 574
QY 601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAEELEVIATHPARDHSFPVDFDNLHXY 660
DB 575 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAEELEVIATHPARDHSFPVDFDNLHXY 634
QY 661 VPRIIQNICTEFNSQPRN 678
DB 635 VPKVQNICTEFNSQPRN 652

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RESULT 6

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Q8K047 PRELIMINARY; PRT; 650 AA.
AC Q8K047;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RIKEN cDNA 2810429K11 gene.
GN VIT OR 2810429K11RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034120; AAH34120.1; -.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 650 AA; 70698 MW; 1641623B11003B48 CRC64;

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Query Match 80.0%; Score 2801; DB 11; Length 650;
 Best Local Similarity 80.5%; Pred. No. 2.5e-192;
 Matches 548; Conservative 40; Mismatches 59; Indels 34; Gaps 5;

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QY 1 MRTVLTMKASVTEMFLVLLVTGVHNSKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIV 60
DB 1 MGIWPTMKASVTEMFLVLLVTGVHNSKETAKKIKRPKFTVPQINCVDKAGKINPEFIV 60

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QY 61 KCPACQDPKHYVGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
Db 61 KCPACQDPKHYVGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
QY 121 VQSLSPWRRESFVILESKPKGGVTPYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSPWRRESFVILESKPKGGVTPYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVATPPTLPRPSPSAATSTSIIPRQSVGHRSQEM---DLWSTATYTS 237
Db 181 PVTLMQLLAVTVATPPTLPRPSPSAATSTSIIPRQSVGHRSQEM---DLWSTATYTS 237
QY 238 QNRPRADPGIQRDPSGAAPQKPGADVSLGLVAPKEELSTQSLVPSLSDGPNCKIDLSP 297
Db 238 QNRPRADPGIQRDPSGAAPQKPGADVSLGLVAPKEELSTQSLVPSLSDGPNCKIDLSP 297
QY 298 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 357
Db 298 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 357
QY 270 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 329
Db 270 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 329
QY 358 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 417
Db 358 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 417
QY 330 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 389
Db 330 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 389
QY 418 RESGINIFPITIEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 477
Db 418 RESGINIFPITIEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 477
QY 390 RESGINVFITVEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 449
Db 390 RESGINVFITVEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 449
QY 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFEISDTDTIGAV 537
Db 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFEISDTDTIGAV 537
QY 538 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 597
Db 538 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 597
QY 510 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 569
Db 510 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 569
QY 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 657
Db 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 657
QY 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 629
Db 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 629
QY 658 HOYVPRIIQNICTEFNSOPRN 678
Db 658 HOYVPRIIQNICTEFNSOPRN 678
QY 630 YKIAPRIIQNICTEFNSOPRN 650
Db 630 YKIAPRIIQNICTEFNSOPRN 650

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RESULT 7

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Q9CY21
ID Q9CY21 PRELIMINARY; PRT; 650 AA.
AC Q9CY21
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE 2810429Klik protein.
GN VIT OR 2810429KLIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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RA Guetincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.,
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL; AK013193; BAB28702.1; -.
DR HSSP; P17301; LAOX.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50334; VWA; 2.
SQ SEQUENCE 650 AA; 70638 MW; 03B4823E111A214B CRC64;
Query Match 79.8%; Score 2796; DB 11; Length 650;
Best Local Similarity 80.5%; Pred. No. 5.7e-192;
Matches 548; Conservative 39; Mismatches 60; Indels 34; Gaps 5;
QY 1 MRTVVLTKASVIEMLVLLVTGVHSHNKETAKKIKRPFTVPQINCVDVAKGKIIDPEFIV 60
Db 1 MGIIVPTMKASVIEVLLVLLVTGHSNKETPKTKRPLKTVQINCVDVAKGKIINPEFIV 60
QY 61 KCPACQDPKHYVGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
Db 61 KCPACQDPKHYVGTDDVYASVSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
QY 121 VQSLSPWRRESFVILESKPKGGVTPYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
Db 121 VQSLSPWRRESFVILESKPKGGVTPYPSALTYSSSKSPAAQAGETTKAYQRPPIPGTTAQ 180
QY 181 PVTLMQLLAVTVATPPTLPRPSPSAATSTSIIPRQSVGHRSQEM---DLWSTATYTS 237
Db 181 PVTLMQLLAVTVATPPTLPRPSPSAATSTSIIPRQSVGHRSQEM---DLWSTATYTS 237
QY 238 QNRPRADPGIQRDPSGAAPQKPGADVSLGLVAPKEELSTQSLVPSLSDGPNCKIDLSP 297
Db 238 QNRPRADPGIQRDPSGAAPQKPGADVSLGLVAPKEELSTQSLVPSLSDGPNCKIDLSP 297
QY 298 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 357
Db 298 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 357
QY 270 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 329
Db 270 IDGSTSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVOYGNPATFNLKTHNSRD 329
QY 358 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 417
Db 358 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 417
QY 330 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 389
Db 330 TAIEKITQGGLSNVGRAISFVTKNFFPSKANGNRSGAPNVVVMVDGWPDKVBEASRLA 389
QY 418 RESGINIFPITIEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 477
Db 418 RESGINIFPITIEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 477
QY 390 RESGINVFITVEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 449
Db 390 RESGINVFITVEGAAREKQVVPENPANKAVCTNGFYSLHVQSWFGLKHTLQPLVKR 449
QY 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFEISDTDTIGAV 537
Db 478 VCDTRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLOFVTNLTKEFEISDTDTIGAV 537
QY 538 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 597
Db 538 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 597
QY 510 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 569
Db 510 QYTYEORLEFGDPKYSKPDILNAIKRVYVSGGTSSTGAALNPALEQLFKSKPKNRK 569
QY 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 657
Db 598 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 657
QY 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 629
Db 570 ILITDGRSVDVRIIPAMAHLKGVITYAIGVAAQAELEVIATHPARDHSPFVDFDNL 629
QY 658 HOYVPRIIQNICTEFNSOPRN 678
Db 658 HOYVPRIIQNICTEFNSOPRN 678

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Db 630 YKIAPRIIIONICTEFNSQPRN 650
RESULT 8
Q8BQ41 PRELIMINARY; PRT; 628 AA.
ID Q8BQ41
AC Q8BQ41
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VITRIN.
GN VIT OR 2810429KJ11RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion;
RC MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK0151606; BAC34688.1; -.
DR MGD; MGI:1921449; Vit.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 628 AA; 68198 MW; C96C4ACB9E72480 CRC64;

Query Match 76.6%; Score 2682; DB 11; Length 628;
Best Local Similarity 77.7%; Pred. No. 8.2e-184;
Matches 529; Conservative 39; Mismatches 57; Indels 56; Gaps 6;

Qy 1 MRTVLTAKASVIEKFLVLLVTGSHNKETAKKIKRPKPTVQINCVDKAGKIIDPEPIV 60
Db 1 MGIIVPTMKASVIEVL-----AVPQINCVDKAGKIIINPEMV 38

Qy 61 KCPAGCQDPKHYVTDVYASVYSCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNG 120
Db 39 KCPAGCQDPKHYVGTGYASVYSCGAAIHSGVLDNSGGKILVRKVAGQSGYKGSYNG 98

Qy 121 VQSLSPWRRESFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPINGITTAQ 180
Db 99 VQSLSPWRRESFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPINGITTAQ 158

Qy 181 PVTLMQLAVTAVATPTTLPRPSPASATTSIPRQSVGHRSQEM---DLWSTATYSS 237
Db 159 PVTLTQAQTPVAEVTHTSTSK--PFAASVTNSPRQPVGHRSQEMEEVDGWK----- 209

Qy 238 QNRPRADPGIORQDPGSGAFAQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLSP 297
Db 210 -----PG-----PVLID--SGFVPKEELSTOSBPVPGQDPNCKIDLSP 247

Qy 298 IDGSTSIKRRPRIOKQLADVAQALDIPAGPLMGVYQYQNDPATFNKTHNSRDLE 357
Db 248 IDGSTSIKRRPRIOKQLADVAQALDIPAGPLMGVYQYQNDPATFNKTHNSRDLE 307

Qy 358 TAIEKIQRGGLSNVGRASIFVTKNPFPSKANGNRSAGPVMVVDGWPTDKVEASRLA 417
Db 308 TAIEKIQRGGLSNVGRASIFVTKNPFPSKANGNRSAGPVMVVDGWPTDKVEASRLA 367

Qy 418 RESGINPFITTEGAENEKQYVVEPNFANKAVCTNGFYSLHVQSFWGLHKTLOPLVKR 477
Db 368 RESGINPFITTEGAENEKQYVVEPNFANKAVCTNGFYSLHVQSFWGLHKTLOPLVKR 427
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Qy 478 VCDTDLACSKTCLNSADIGFVIDGSSSVGNGFNFTVLQFVTNLTKPEISDITTRIGAV 537
Db 428 VCDTDLACSKTCLNSADIGFVIDGSSSMGTSNFTVLQFVANLSKEPEISDITTRIGAV 487

Qy 538 QYTYEORLEFGPKYSKPKDILNAIKVGVYWSGGTSTGAALNFALBQLFKSKPKNRKLM 597
Db 488 QYTYEORLEFGPKYNSKADILLSAIRRVGWSGGTSTGAALQYALBQLFKSKPKNRKLM 547

Qy 598 ILITDGRSYDDVRIPAMAHLKGVITYAIGVAMAAQBELEVIATHPARDHSFFVDFPNL 657
Db 548 ILITDGRSYDDVRIPAMAHLKGVITYAIGVAMAAQBELEVIATHPARDHSFFVDFPNL 607

Qy 658 HQYVPRIIIONICTEFNSQPRN 678
Db 608 YKIAPRIIIONICTEFNSQPRN 628

RESULT 9
Q8AW56 PRELIMINARY; PRT; 553 AA.
ID Q8AW56
AC Q8AW56;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SI:D2234G15.4 (Novel protein similar to coagulation factor C homolog
DE (Cochlin, COCH)).
GN SI:D2234G15.4.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Babbage A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL596026; CAD58748.1; -.
DR InterPro; IPR004043; LCCL.dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 553 AA; 60351 MW; 4A3B136747C488P0 CRC64;

Query Match 33.9%; Score 1187.5; DB 13; Length 553;
Best Local Similarity 37.7%; Pred. No. 1.3e-76;
Matches 251; Conservative 107; Mismatches 184; Indels 123; Gaps 8;

Qy 16 FLVLVLTGVHS-----NKETAKKIKRPKPTVQINCVDKAGKIIDPEFIVKCPAGCQDPKY 71
Db 5 FAVLVLTGVLSLWCTSGSELNVA TP-----ISGTRAVDLSDTHLVLCFANCSLWSL 58

Qy 72 HVGTDVYASVYSCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSPWR 131
Db 59 SVFGSGVYASVYSCGAAIHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSPWR 118

Qy 132 SFVLESKPKKGVTPSALTYSSKSPAAQAGETTKAYORPPITGTAQPTLMQLAVT 191
Db 119 SF----- 120

Qy 192 VAVATPTTLPRPSPASATTSIPRQSVGHRSQEMDLWSTATYSSQNRPRADPGIOR 251
Db 121 -TVARTISLPLEVSSQTSSTSAIV----- 142

Qy 252 PSGAFAQKPGVADVSLGLVPKEELSTOSLBPVSLGDPNCKIDLSPIDGSTSIKRRPRI 311
Db 143 ASGAA-KKPVKK-----IVKK-----PPATAHKDCPVDMLLDSSVYNGQRFPNL 188
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QY 312 QKOLLADVAQALDTPAGPAGVGVQYQGNPNATHFNKLTHTNSRDLKTAIEKITORGGLSN 371
Db 189 QKNFVSKLMLKVTGQPHVGVQYQGNPNATHFNKLTHTNSRDLKTAIEKITORGGLSN 248
QY 372 VGRALSFVTKNPFKANGNSGAPNVAVMVDGPTDKVEASRLARESGINIPFITIEG 431
Db 249 TGKAILHTVRPFSPDFGVRGYPYVIVFVWGNPNDVNEAAILARESGINIPFVSAK 308
QY 432 AARENEKQYVWBPFPNFAKAVCTRTNGFYSLVHVSFVGLHKTLOPLVKRVCDTDLACSKTCL 491
Db 309 PSPBEASLVSDQDFRKAACKNEFTFTMSFVFNKFPVLAQKLSIDQMLCKTICY 368
QY 492 NSADIGFVIDSSSGVGTGNFTVLQFVNTLKEFEISDTRIGAVQYTYEORLEFGDK 551
Db 369 NSVDLGLFIDSSSGVGTGNFTVLQFVNTLKEFEISDTRIGAVQYTYEORLEFGDK 428
QY 552 YSSKPDILNAIKRVYMGSGTSTGAINFALFOLFKKPKKPKKLMILITDGRSYDDVRI 611
Db 429 HVLKDNALRALQKIPYMGSGTATGDAINFARSLPKPRSSNRKPLIITDQSYDDVRI 488
QY 612 PMAAHLKGVITYAIGVAAQAELEVIATHPARHSPFVDFDNLHNVVPRIIQNIC-- 669
Db 489 PMAAQRGIVYAVGVAAWAPMEDLKAMASEKESHVFTTFTGLQGFQOPVIRGICRD 548
QY 670 -TEFN 673
Db 549 FTEFN 553

RESULT 10
Q961U6 PRELIMINARY; PRT; 494 AA.
AC Q961U6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Coagulation factor C (Limulus polyphemus) homolog (Cochlin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007230; AAH07230.1; -.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWFA; 2.
SQ SEQUENCE 494 AA; 53230 MW; 9920BEF97A0AF2FF CRC64;

Query Match 29.1%; Score 1017.5; DB 4; Length 494;
Best Local Similarity 37.2%; Pred. No. 1.7e-64;
Matches 214; Conservative 90; Mismatches 153; Indels 119; Gaps 7;

QY 44 INCVDKAGKIIDPEPIVKPCAGQDPKVVHVTGVYASVSSVCGAAVHSGVLNDSGGKIL 103
Db 32 ITCFTRGIDIRKKEADVLCPGECPLSEFSVGNIVIASVSSICGAAVHRGVINSGGPVR 91
QY 104 VRKVGQSGYKSGVNGVQSLSPWRBSFVLESKPKKGVITYPSALYSSKSPAAQAG 163
Db 92 VYSLPGRENVSDANGIOSQMLSEWSASFVTKCK-----SSTQEATQA- 137
QY 164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTAVATPTLPRPSPSAATSTIPRPSQVGRHS 223
Db 138 -----VSTAHF----- 143

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QY 224 QEMDLWSTATYTSQNRPRADPGIQODPSGAAFQKPVGADVSLGLVPKKEELSTQSLPVP 283
Db 144 -----PTGRRLKK-----TPEKK----- 156
QY 284 SLGDPNCKIDISFLIDGSTSGKRFRIOKQLLADVAQALDTPAGPAGVGVQYQGNPNAT 343
Db 157 -TGNQDKADIAFLIDGSGFNIGQRNFKQKPVGVKVALMLGIGTEGPHVGLVQASBHPKI 215
QY 344 HFNLTHTNSRDLKTAIEKITORGGLSNVRGAI SFVTKNPFKANGNSGAPNVAVMVD 403
Db 216 EFLKNFTSAKDLVFAIKVEGFRGNSNTGKALKHTAQKFTFVDAGVRKGIPIKVVVFPID 275
QY 404 GWPTDKVEASRLARESGINIPFITIEGAANEKQYVWBPFPNFAKAVCTRTNGFYSLVHVS 463
Db 276 GWPSDIEEAGIVAREFGVNVFIVSAKPIPEELGWQVDVTFVDKAVCAKRNNGFPFVHMPN 335
QY 464 WFLHKTLOPLVKRVCDTDLACSKTCLNSADIGFVIDSSSGVGTGNFTVLQFVNTLTK 523
Db 336 WFGTTKYVKPLVQKLCITHEQMMCSKTCTNSVNIAPFLIDGSSSGVSDSNFRLMLEFVSNIAK 395
QY 524 RFEISDTRIGAVQYTYEORLEFGDKYSSKPDILNAIKRVYMGSGTSTGAINFALF 583
Db 396 TFEISDIGAKAAVQFTYDQRTPEFTDSTYKENVLAVIRNYMGSGTATGDAISFTVR 455
QY 584 QLEFK--KSKPNRKLMLITDGRSYDDVRIPAMAHAH 617
Db 456 NVFGPIRESPNK-NFLVIVTDQSYDDVQGPAAAH 490

RESULT 11
Q7SYTS PRELIMINARY; PRT; 490 AA.
AC Q7SYTS;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H.C., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshilyuk S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.J., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;

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Search completed: May 27, 2004, 16:47:03
Job time : 54 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:44:13 ; Search time 23 Seconds
(without alignments)
1521.844 Million cell updates/sec

Title: US-10-063-688-34
Perfect score: 3502
Sequence: 1 MRTVLTAKASVIEMLVLL.....QYVRIIQTCTFNSQPN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1129.5	32.3	550	4	US-09-907-794A-227
2	1129.5	32.3	550	4	US-09-905-125A-227
3	1129.5	32.3	550	4	US-09-902-775A-227
4	501.5	14.3	496	1	US-08-462-128-37
5	501.5	14.3	496	1	US-08-463-180-37
6	501.5	14.3	496	2	US-08-001-078A-1
7	501.5	14.3	496	2	US-08-897-443-4
8	501.5	14.3	496	2	US-08-463-218-1
9	501.5	14.3	496	5	PCT-US94-00253-1
10	370	10.6	915	4	US-09-907-794A-34
11	370	10.6	915	4	US-09-905-125A-34
12	370	10.6	915	4	US-09-902-775A-34
13	337.5	9.6	956	2	US-08-897-443-3
14	266	7.6	2050	2	US-08-347-594A-2
15	266	7.6	2813	4	US-09-381-261A-1
16	263.5	7.5	638	2	US-08-897-443-1
17	262	7.5	481	4	US-09-914-259-36
18	251	7.2	486	4	US-09-914-259-35
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20	248.5	7.1	452	4	US-09-914-259-34
21	243.5	7.0	2813	3	US-08-896-445A-2
22	243.5	7.0	2813	3	US-08-132-652-2
23	232	6.6	216	4	US-09-795-872-5
24	232	6.6	405	4	US-09-312-283C-374
25	231	6.6	187	2	US-08-177-109A-61
26	231	6.6	187	2	US-08-687-706-61
27	231	6.6	435	5	PCT-US95-04439-1

28 231 6.6 1152 2 US-08-476-062A-43
29 231 6.6 1152 5 PCT-US96-01314-43
30 231 6.6 1152 6 5424399-2
31 231 6.6 1153 1 US-08-173-497-3
32 231 6.6 1153 1 US-08-286-889-3
33 231 6.6 1153 1 US-08-485-618-3
34 231 6.6 1153 1 US-08-362-652-3
35 231 6.6 1153 2 US-08-685-672-3
36 231 6.6 1153 2 US-08-482-293A-3
37 231 6.6 1153 2 US-08-943-363-3
38 231 6.6 1153 3 US-09-193-043-3
39 231 6.6 1153 4 US-09-688-307A-3
40 231 6.6 1153 4 US-09-350-259-3
41 228 6.5 1163 2 US-08-476-062A-44
42 228 6.5 1163 5 PCT-US96-01314-44
43 225 6.4 1163 1 US-08-173-497-4
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45 225 6.4 1163 1 US-08-485-618-4

ALIGNMENTS

RESULT 1

US-09-907-794A-227
; Sequence 227, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Raton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas P.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907.794A

; CURRENT FILING DATE: 2001-07-17

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547


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; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-227

Query Match      32.3%; Score 1129.5; DB 4; Length 550;
Best Local Similarity 37.1%; Pred. No. 2.8e-97;
Matches 234; Conservative 103; Mismatches 175; Indels 119; Gaps 7;

QY 44 INCVDKAGKIIDPEFIVKCPAGCQDPKYHVYGTDDVYASVSSVCGAAVHSGVLDNSGGKIL 103
Db 32 ITCTFRGLDIRKEKADVLCPCGCPLEEFVSIGNIVYASVSSICGAAVHRGVINSGGPVR 91
QY 104 VRKVAGQSGYKGSYNGVQSLSLPRWRBSFVLESFKPKGVTPYSALTYSKSPAAQAG 163
Db 92 VYSLPGRNYSVDANGIQSOMLSRWSASFVTKGK-----SSTQEQATGQA- 137
QY 164 ETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHR 223
Db 138 -----VSTAHF----- 143

QY 224 QEMDLWSTATYTSSQNRPRADPGIQODPFGAFAQKPGVADVSLGLVPKBEELSTQSLP 283
Db 144 -----PTGKRLKK-----TPEKK----- 156
QY 284 SLGDPNCKIDLSFLDGSSTSGKRFRIOKQLLADVAQALDIGPAGPLMGVVYQYGDNPAT 343
Db 157 -TGNKDCKADIAFLDGSFNGISREFNQKPNFVKVQVLMGLIGTSGPHVGLVQASEHPKI 215
QY 344 HFNLTHTNSRDLKTAIEKIQRGSLSNVGRASFTVKNFPSKANGNSGAPNVVVWVD 403
Db 216 EFLKNTFSAKDVLPAIKVGVGRGNSNTGKALKHTAOKPFTVDAGVRKGIPIKVVVVVFID 275
QY 404 GWPTDKVEASRLARESGINIPFIETGAABNEKQVVPENFANKAVCKRTNGFYSLHVQS 463
Db 276 GWPSDDIEAGIVAREFGVNVFIVSAKPIPELGMVQDVTVDKAVCKNNGFFSYHMPN 335
QY 464 WFLGHTLQPLVKRVCDTRDLACSKTCLNSADIGFVLDGSSSVGTGNFRTVLQFVYTNLTK 523
Db 336 WFGTTKYVKPLQKLCVTHEQMCKSKTCVNSVNI AFLDGSSSVGDSPNFRMLLEFVSNI 395
QY 524 EPEISDTRIGAVQYTEORLEFQDKYSKSPDILNAIKRVYWSGGTSTGAAINPALE 583
Db 396 TPEISDIGAKIAAQQTYDQRTFSDYSTYKENVLAVIRNIRYNSGGTATGDAISFTVR 455
QY 584 QLFK--KSKPNKRLMILITDGRSYDDVRI PAWAHLKGVITVAIGVAAAOEELEVIAT 641
Db 456 NVFGPIRSPNK-NFLVIVTDGQSYDDVQGPAAAHADAGITTFSGVAVAWAPLDDLDKMAS 514
QY 642 HPARDHSPFVDFDMLHQVTPRIQNICTEF 672
Db 515 KPESHAFTRFTGLEPIVSDVIRGICDFP 545

RESULT 3
US-09-902-775A-227
; Sequence 227, Application US/05902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```



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QY 224 QEMDLNSTATYTTSSQNRPRADPGIQRDPSGAAPQKPVGDVSLGLVPKEELSTQSLBPV 283
Db 144 -----PGKRLK-----TPEKK-----156
QY 284 SLGDPNCKIDLFLIDGSTSIGRRFRIOKOLLADVAQAALDIGPAGPLMGVQVQGNPAT 343
Db 157 -TGKCKCKADIAFLIDGSNIGQRRLQNFVKVLMIGIGTEGPHGLVQASHPKI 215
QY 344 HFNLTHTNSRDLKTAIEKIQGGSLNVGRAISFVTKNFFSKANGNRSGAPNVVVVMD 403
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QY 524 EPEISDTRIGAVQVYTBORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAALNPALE 583
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QY 584 QLPK--KSKNKKMLILITDGRSYDDVRIPAMAHLKGVITYAIGVANAQAQEELEVIAT 643
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QY 642 HPARDHSFVDEPDNLHQVYVPRIIQNICTEP 672
Db 515 KPESHAPFTREPTGLEPIVSDVIRGICRDP 545
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RESULT 4

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US-08-462-128-37
; Sequence 37, Application US/08462128
; Patent No. 5686059
; GENERAL INFORMATION:
; APPLICANT: Goetnick, Paul F.
; APPLICANT: Tondravi, Mehrdad
; TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/462,128
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: US 07/866,403
; FILING DATE: 10-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 496 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-462-128-37
;
; Query Match 14.3%; Score 501.5; DB 1; Length 496;
; Best Local Similarity 28.8%; Pred. No. 2.8e-38; Indels 61; Gaps 9;
; Matches 129; Conservative 80; Mismatches 178;
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; QY 273 HELSTQSLPVSIGDPNCK---IDLSPIDGSTSIGRRFRIOKOLLADVAQAALDIGPAG 329
; Db 19 QALCSFCLAPQSRGH-LCTRPTDLPVVDSSSRVPEFEKVKVFLSQVIESLDVGN 77
; QY 330 PLMGVVOYQGNPANTHNLKTHNTRDLKTAIEKIQGGSLNVGRAISFVTKNFPKANG 389
; Db 78 TRGVNMYASTVRQEFSLRAHVAKALLQAVRRIQPLSTGTMTGLAIQPAITTKAFG 137
; QY 390 NRGGAN---VVVWVDGMPDQKVEASRLARSGINIPFITTEGAENE--KQVYVPEPN 444
; Db 138 GRSRSPDISKVIIVVTDGRPDQSVQVDSARASGVLELPAIGV-GSYDKATLRQIASEPQ 196
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; Db 197 DEHVD-----YVBSYSVIEKLSRKQEAFCVVDLDCATGDHCEQVCISSPG 246
; QY 494 -----ADIGFVIDGSSSVGTGNFRITVLOPVTNLTKEPF 526
; Db 247 CACHGFTLNSDGKTCNVCSGGGSSATDLVFLIDGSKSVRPFELVKKPISQIVDTLD 306
; QY 527 ISDTRIGAVQVYTBORLEFGDKYSSKPDILNAIKRVGWSGGTSTGAALNPALEOLF 586
; Db 307 VSDKLAQGLVQYSSSVRQEPFLGRFHTTKDIIKAAVRNMSYMEKGTWTGALKYLDNSP 366
; QY 587 KKS---KPNRKKMLILITDGRSYDDVRIPAMAHLKGVITYAIGVANAQAQEELEVIATHP 643
; Db 367 TVSSGAPGAQGVIVPTDGRSQDYINDAAKAKDLGFKMFAVGVGNVABDELEIASEP 426
; QY 644 ARDHSFVDEPDNLHQVYVPRIIQNICTE 671
; Db 427 VASHYFTADFTKIQIGKKLQKKICVE 454
;
; RESULT 5
; US-08-463-180-37
; Sequence 37, Application US/08463180
; Patent No. 5741670
; GENERAL INFORMATION:
; APPLICANT: Goetnick, Paul F.
; APPLICANT: Tondravi, Mehrdad
; TITLE OF INVENTION: CARTILAGE MATRIX PROTEIN AND METHODS FOR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lahive & Cockfield
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,180
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/006,096
; FILING DATE: 15-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
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Query Match      10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 1.9e-25;
Matches 139; Conservative 81; Mismatches 191; Indels 364; Gaps 13;

Qy 256 AFQKPGVADVSLGLVPKEELSTQSLPVSGLGDPNCKIDLSFLIDGSTSIGKRRPRIQKOL 315
Db 23 ARERSGRSISRGRHARTHPTQALLS---SCENKRALDVFIIIDSSRSVNTHDYAKVKEP 79
Qy 316 LADVAQALDIDGAPGLMGVQYGDNPATHPNLTHTNSRDLKTAIEKITQGGLSNVGRA 375
Db 80 IVDILQPLDIDGPDVTRVGLLQYGSTVKNEFSLATPKRKSERVAERVMRHLSTGTMTGLA 139
Qy 376 ISFVTNPFKSKANGN---RSGAPNVVVVMDGHPDTPDKVEASRLARESGINIF----- 425
Db 140 IOYALNIAFSAEAGARPLRENVPRVIMIVTDGRPODSVAEVAARAKARDTGLIFAGVGQV 199
Qy 426 -FTTIE--GAENKEQVVVEPNF----- 445
Db 200 DFNTLKSIGSEPHEDHVFVANFNSQIETLTSVQKCLKTAHMCSTLEHNCNHFICINPGS 259
Qy 446 -----ANKAVCR----- 452
Db 260 YVCRCKGYILNSDQTCRIQLDCAMEHDHNCBQLCVNVPGRSFVQCYSGYALAEADGRCV 319
Qy 453 -----TNGFSLHVQSWFGL----- 467
Db 320 AVDYCASENHGCHECVNADGSLYCQCHGFALNPDEKCTTRINYNALNKPCCHEBCVNM 379
Qy 468 -----HK--TLQP-----LV----- 475
Db 380 EESYCRCHRGYTLDPNGKTCRVDHCAQDHCGBQLCLNTEDSFVQCQSGFLINEDLK 439
Qy 476 ----- 475
Db 440 TCSRVDYCLLSDHCEYSVNMDSRSPACQPEGHVLSGDKTCAKLDSCALGDHGCHEHC 499
Qy 476 ----- 475
Db 500 VSSSDSPVQCFCFGYTLREDGKTCRRKDVQQAIDHGCEHICVNSDDSYTCELEGPRLAE 559
Qy 476 -----KRVCDTDLRACSKTCLNSA-----DIGFVI 500
Db 560 DGRCKRKOVCKSTHHCCEHICVNGNSYICKSBEFVLAEADGRCKKCTGEGFDLVFVI 619
Qy 501 DGSSTVGTGNFRFVLPVNTLTKFEFISDTRIGAVQYTYEQRLBFGDPKYSKPDILN 560
Db 520 DGSKSLGEENFEVQKVPVGTGIDSLTISPKAARVGLLQYSTQVHTBTPLNFSNKAQDKK 679
Qy 561 AIKRVGWSGTGTGAINFALBQLFKK---SKPNKRL---MLITDGRSYDDVRIPAM 614
Db 680 AVAHMTYMGKSGMTGLALKEMFERSFTQGEARPLSTRVPRAAIVFTDGRAQDDVSEWAS 739
Qy 615 AAHLKGVITVYAGVMAAARELEVIAHPARDHSFFVDEPDNLHGYVPRILIONIC 669
Db 740 KAKANGITMTAVGVKAIBELOEIASBPTNKLHYAEDFSTWDEISEKLKKGIC 794

RESULT 11
US-09-905-125A-34
; Sequence 34, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Denoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
```

```
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-905-125A-34
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Query Match      10.6%; Score 370; DB 4; Length 915;
Best Local Similarity 17.9%; Pred. No. 1.9e-25;
Matches 139; Conservative 81; Mismatches 191; Indels 364; Gaps 13;

Qy 256 AFQKPGVADVSLGLVPKEELSTQSLPVSGLGDPNCKIDLSFLIDGSTSIGKRRPRIQKOL 315
Db 23 ARERSGRSISRGRHARTHPTQALLS---SCENKRALDVFIIIDSSRSVNTHDYAKVKEP 79
Qy 316 LADVAQALDIDGAPGLMGVQYGDNPATHPNLTHTNSRDLKTAIEKITQGGLSNVGRA 375
Db 80 IVDILQPLDIDGPDVTRVGLLQYGSTVKNEFSLATPKRKSERVAERVMRHLSTGTMTGLA 139
Qy 376 ISFVTNPFKSKANGN---RSGAPNVVVVMDGHPDTPDKVEASRLARESGINIF----- 425
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Db 140 IYALNIAFSEAEGRPIRENVPRVIMIVTDGRPODSVAEAAKARDTGILFAIGVGQV 199
Qy -FITIE--GAANEKQYVVEPNF----- 445
Db 200 DFNTLKISGSEPHEDHVLVAFNSQIETLTSVFQKCLTAHMCSTLEHCAHFCINIPGS 259
Qy -FITIE--GAANEKQYVVEPNF----- 452
Db 260 YVCRCKQGYILNSDQTTCTRIQDLCAEDHNCBQLCVNVPSPVCCYSGYALAEDEKRCV 319
Qy -FITIE--GAANEKQYVVEPNF----- 467
Db 320 ADVYCASNHGCEHCYNADGSLYCQCHGFAINDEKTCRINVCALNKPGECEHCVM 379
Qy -FITIE--GAANEKQYVVEPNF----- 475
Db 380 EESYVCRCHRGYTLDPNGKTCRVHDCAQDHCQGLCINTEDSPVCCSEGFILNEDLK 439
Qy -FITIE--GAANEKQYVVEPNF----- 475
Db 440 TCSRVDYCLLSHDGCEYSCVNDRSFACQCPGHEVLRSDGKTCAMLDSCALGDHGEHSC 499
Qy -FITIE--GAANEKQYVVEPNF----- 475
Db 500 VSSEDSFVCCFEGYILREDGKTCRKDVQCAIDHGCEHICVNSDDSYTCSEGLEFRLA 559
Qy -FITIE--GAANEKQYVVEPNF----- 500
Db 560 DGKCRKRDVCKSTHGHCEHICVNGNSYICKSEGFVLAEDGRCKCTGEPDILVFI 619
Qy -FITIE--GAANEKQYVVEPNF----- 501
Db 501 DGSSVGTGRTVQLVFNLTKEFEISDVTDRIGAVQYTYEQRLEFGDFKYSSKPDILN 560
Qy -FITIE--GAANEKQYVVEPNF----- 620
Db 620 DGKSLGEENFEWKQFVTGIIDSLTSPKAAVGLLQYVQVHTPTLRNFNSAKDMKK 679
Qy -FITIE--GAANEKQYVVEPNF----- 561
Db 561 AIKRVGTSGTSTCAINPALEQLFKK---SKWKRKL---MILITGRSYDDVRIIPAM 614
Qy -FITIE--GAANEKQYVVEPNF----- 680
Db 680 AVAHMYKMGKSMGTGLAKHGFERSPTQGEARPLSTRVPRAAIVFTDGRAQDDVSEWAS 739
Qy -FITIE--GAANEKQYVVEPNF----- 615
Db 615 AAHLKGVTVYGAIVMAAOELEVIAHPARDHGFVDFEFTNLHGYVPRITONIC 669
Qy -FITIE--GAANEKQYVVEPNF----- 740
Db 740 KAKANGITWYAVGVKAIEERLOEIAEPTNKHLPYAEDEFSTMDIEISKLKKGIC 794

RESULT 12

US-09-902-775A-34
; Sequence 34, Application US/09902775A
; Patent No. 6686451

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Pao, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,775A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 34
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-34

Query Match 10.6%; Score 370; DB 4; Length 915;

Best Local Similarity 17.9%; Pred. No. 1.9e-25;

Matches 139; Conservative 81; Mismatches 191; Indels 364; Gaps 13;

Qy 256 AFQKPGVADVSLGLVPKEELSTQSLPVSGLDPPNCKIDLSPLIDGSTSGKRRFRQKOL 315
Db 23 ARESRGRSISGRHARHPQTALLES---SCENRADLVFIIDSSRVNTHDYAKKEP 79
Qy 316 LADVAQALDIGPAGPLMGVQVQYNDNPATHFNLKHTNSRDLKTAIEKIFQRGSLNVGRA 375
Db 80 IVDILQFLDIGDPVTRVGLLQYGVSTVKNFSLKTFKRSSEVERAVKRMHLSGTGTGLA 139
Qy 376 ISFTYONPFSKANGN---RSGAPNVVVVVDGWPTDKVBEASRLARESGINIF----- 425
Db 140 IQYALNIAFSEAEGRPIRENVPRVIMIVTDGRPODSVAEAAKARDTGILFAIGVGQV 199
Qy 426 -FITIE--GAANEKQYVVEPNF----- 445
Db 200 DFNTLKISGSEPHEDHVLVAFNSQIETLTSVFQKCLTAHMCSTLEHCAHFCINIPGS 259
Qy 446 -----ANKAVCR----- 452
Db 260 YVCRCKQGYILNSDQTTCTRIQDLCAEDHNCBQLCVNVPSPVCCYSGYALAEDEKRCV 319
Qy 453 -----TNGFYSLHVQSWFGL----- 467

APPLICANT: Richter, Tamar
TITLE OF INVENTION: CLONING AND PRODUCTION OF HUMAN VOM
TITLE OF INVENTION: WILLEBRAND FACTOR GPID BINDING DOMAIN POLYPEPTIDES AND
TITLE OF INVENTION: METHODS OF USING SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,594A
FILING DATE: No. 5849536member 30, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2050 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-347-594A-2

Query Match 7.6%; Score 266; DB 2; Length 2050;
Best Local Similarity 21.9%; Pred. No. 4.6e-15;
Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps 19;

QY 250 QDPGAAFPKPVGADVSLGLVPKEELSTQSLPEVSLGDPNCK--IDLSFLIDGSTSIGR 307
DB 475 QEPGLV--PPTDAPVSPPTLYVEDIS----EP-PLHDFYCSRLLDVFLDGGSSRLSEA 528
QY 308 RFRIQKQLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAIEKITQ 367
DB 529 EFVILKAPVVDMMERLRISSQWVRVAVVEYHDSHAYIGLKORRPSRLRIASQVKYAG 588
QY 368 G-LSNVGRAISFVTKNPFKSKANGNRSGAPNVVVMVDGMPDKVKEASRLARESGINIF 426
DB 589 SQVASTSEVLKYTLFQIFSKI--DRPEASRIALLMAS-----QEPQMSRN-----FV 635
QY 427 ITTEGAARENEKQYVVEP-----NPAKAVCKRTNGFYSLHVSQWFLGHTLOPL 474
DB 636 RYVQGL--KKKQVIVPVGIGPHANLQIRLIEKQAPENKAPVLSVDE---LEQQRDEI 690
QY 475 VKRVCDTDLRLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
DB 691 VSYLCDLAPAPPTLPDPAQVTVGPGLLGVSTLGPKNRSMWLDVAFVLEGSDKIGRAD 750
QY 511 FRTVLPQVTLTKPEFISDTRIGAVQYTYEORLEFGDFKYSSKPDILNAIKRVGYWSG 570
DB 751 FNRSKFMEEVQIRMVDVQDSIHVTVLQYSYMTVVEYFPFSAQSGDILQVRVREIRYQGG 810
QY 571 G-TSTGAALNFALEBOLFKSKPKNRK---LMILITDGRSYDDV-RIPAMAHLKGVTYA 625
DB 811 NRTNTGLALRYLSHSLVSGDREQAPNLVYMTGNPASDEIKRLPG-----DIQVVP 864
QY 626 IGVAWAAQ--BELEVIATHPARDHSFFVDEDFONLHQYVPRIIQNIC 669
DB 865 IGVGNPNVQELERIGWFNA---PILIQDFETLPREAPDLVLQRC 906

RESULT 15
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; Sequence 1, Application US/09381261A
; Patent No. 6489290
; GENERAL INFORMATION:
; APPLICANT: Loscalzo, Joseph
; APPLICANT: Imbal, Aida
; TITLE OF INVENTION: No. 6489290el Anti-Platelet Agent
; FILE REFERENCE: 102258.327
; CURRENT APPLICATION NUMBER: US/09/381.261A
; CURRENT FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: PCT/US98/06092
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/046,981
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2813
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-381-261A-1

Query Match 7.6%; Score 266; DB 4; Length 2813;
Best Local Similarity 21.9%; Pred. No. 7.9e-15;
Matches 102; Conservative 85; Mismatches 200; Indels 78; Gaps 19;

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DB 1238 QEPGLV--PPTDAPVSPPTLYVEDIS----EP-PLHDFYCSRLLDVFLDGGSSRLSEA 1291
QY 308 RFRIQKQLADVAQALDIGPAGPLMGVQYGDNPATFNKLTHTNSRDLKTAIEKITQ 367
DB 1292 EFVILKAPVVDMMERLRISSQWVRVAVVEYHDSHAYIGLKORRPSRLRIASQVKYAG 1351
QY 368 G-LSNVGRAISFVTKNPFKSKANGNRSGAPNVVVMVDGMPDKVKEASRLARESGINIF 426
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QY 427 ITTEGAARENEKQYVVEP-----NPAKAVCKRTNGFYSLHVSQWFLGHTLOPL 474
DB 1399 RYVQGL--KKKQVIVPVGIGPHANLQIRLIEKQAPENKAPVLSVDE---LEQQRDEI 1453
QY 475 VKRVCDTDLRLACSKTC-----LNS--ADIGFVIDGSSSVGTGN 510
DB 1454 VSYLCDLAPAPPTLPDPAQVTVGPGLLGVSTLGPKNRSMWLDVAFVLEGSDKIGRAD 1513
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DB 1514 FNRSKFMEEVQIRMVDVQDSIHVTVLQYSYMTVVEYFPFSAQSGDILQVRVREIRYQGG 1573
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QY 626 IGVAWAAQ--BELEVIATHPARDHSFFVDEDFONLHQYVPRIIQNIC 669
DB 1628 IGVGNPNVQELERIGWFNA---PILIQDFETLPREAPDLVLQRC 1669

Search completed: May 27, 2004, 16:48:34
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:44:54 ; Search time 48 Seconds
(without alignments)
3944.399 Million cell updates/sec

Title: US-10-063-688-34

Perfect score: 3502

Sequence: 1 MRTVLTWASVIEFLVLL.....QYPRITQICTEPTNSQPN 678

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3502	100.0	678	9	US-09-989-723-179
3	3502	100.0	678	9	US-09-989-729-179
4	3502	100.0	678	9	US-09-989-727-179
5	3502	100.0	678	9	US-09-989-731-179
6	3502	100.0	678	9	US-09-989-732-179
7	3502	100.0	678	9	US-09-991-073-179
8	3502	100.0	678	9	US-09-990-442-179
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41	3502	100.0	678	10	US-09-997-628-179	Sequence 179, App
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43	3502	100.0	678	10	US-09-989-729A-179	Sequence 179, App
44	3502	100.0	678	10	US-09-997-349-179	Sequence 179, App
45	3502	100.0	678	10	US-09-997-440-179	Sequence 179, App

ALIGNMENTS

RESULT 1

US-09-989-722-179
; Sequence 179, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

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Db 121 VQSLSLPRWRESPIVLSKPKKGVYTPSALYSSKSPAAQAGETTKAYQRPPIGTTAQ 180
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Db 181 PVTLMQLLAVTVATPTLPRPSPSAATTSIPRQSVGHRQBMDLWSTATTYSSQNR 240
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Db 241 PRADPGIORQDPGAAQKPKVGAQVSLGLVPEELSTQSLPVSIGDPNCKIDLSPLIDG 300
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Db 301 STSICKRRFRIOQLADVAQALDIPAGPLMGVVGVDNPNATHPNLKTHTNSRDLKTAI 360
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RESULT 2

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; Sequence 179. Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09989,723
; CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C36
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; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
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DB 61 KCPAGCQDPKYHVYGTVDVYASYSSVCGAAVHSGVLNDSGGKILVRKVAQSGYKGSYSNG 120
QY 121 VQSLSLPWRESFVLESKPKKGVTPSALTYSSSKSPAAAGETTKAYQRPPIPGTTAQ 180
DB 121 VQSLSLPWRESFVLESKPKKGVTPSALTYSSSKSPAAAGETTKAYQRPPIPGTTAQ 180
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DB 181 PVTLMQLLAVTVAVATPTTLRPPSPSAASTTSIPRQSVGHSRQEMDLWSTATYSSQNR 240
QY 241 PRADPGIORQDPGSGAAFOKPVGADVSLGLVPKEELSTQSLPVSGLDPNCKIDLSPLIDG 300
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QY 301 STSICKRRFRIOKQLLADVAQALDIPAGPLMGVYQYGDNPATPHNLKTHNSRDLKTAI 360
DB 301 STSICKRRFRIOKQLLADVAQALDIPAGPLMGVYQYGDNPATPHNLKTHNSRDLKTAI 360
QY 361 EKITORGGLSNVGRAISFVTKNPFPSKANGNRSGAPNVVVMVDGWPTDKVBEASRLARES 420
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DB 421 GINIFPITIIEGAANEKQYVVEPNPANKAVCTNGTFYSLHVQSWFGLHKTLOPLVKRVCD 480
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DB 481 TDLRACSKTCLNSADIGFVIDGSSVCGNFTVLQFTNLTKPEISDPTDRIGAVQYT 540
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
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Db	61	KCPAGCQDPKPHVYGTVDVYASYSVSCGAAVH	SGVLDNSGGKILVRKVAGQSGYKGSYNG	120	
Qy	121	VQSLSLPRWRESPTVLSRSPKCKGVYTPSALT	YSSSKSPAAQGETTKAYQRPPITGTTAQ	180	
Db	121	VQSLSPRWRESPTVLSRSPKCKGVYTPSALT	YSSSKSPAAQGETTKAYQRPPITGTTAQ	180	

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Db	361	EKITQRGSLNV	GRAISFVTKN	PFSSKANGNR	SAGPNVVVMV	DGFTDKVBEAS	RLARES	420	
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Db	421	GINIFFITIEGA	ARENKOYVBP	PNFANKAVCR	TNGPYSLHV	QSWFGLHKT	LOPLVVR	480	
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Db	481	TDLRACSKTCL	NSADI	IGFVIDGSS	SVGTGNF	TVLQFVTNL	TKBEFISD	TDTRIGAVQYT	540
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Db	541	YEORLEFGFDK	YSKPDILNAI	KRVGTWS	CGTSTGAAI	NFALBQLFKES	KENKRLMLIL	600	
Qy	601	TDGESYDDVRI	PMAAHLKGV	ITTAIVAMA	AQEELE	VIAITHPARDH	SFFVDFE	PNLHQY	660
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: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Denoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
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: APPLICANT: Gertslien, Mary E.
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: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
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: APPLICANT: Paoni, Nicholas F.
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: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
:
: TITLE OF INVENTION: Secreted and Traz
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: FILE REFERENCE: P2703P1C70
: CURRENT APPLICATION NUMBER: US/09/989
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE:	1998-06-12
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;; PRIOR APPLICATION NUMBER: 60/090863
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;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KCPAGCQDPKHYVGTVDVYASVSCGAAVHSGVLDNSGKILVRKVAGSGYKGSYNG 120

QY 121 VQSLSLPRWRRESFVLESKPKGVTPSALTYSSKSPAAQAGETTKAYORPIPGTTAQ 180
DB 121 VQSLSLPRWRRESFVLESKPKGVTPSALTYSSKSPAAQAGETTKAYORPIPGTTAQ 180

QY 181 PVTLMOLLAVTVAVATPTTLPRPSPAASTTSIPRPSQVGRHSQEMDLSTATYTSQNR 240
DB 181 PVTLMOLLAVTVAVATPTTLPRPSPAASTTSIPRPSQVGRHSQEMDLSTATYTSQNR 240

QY 241 PRADPGIORDPGSAFQKPVGADVSLGLVPKBEELSTQSLPVSGLDPNCKIDLFLIDG 300
DB 241 PRADPGIORDPGSAFQKPVGADVSLGLVPKBEELSTQSLPVSGLDPNCKIDLFLIDG 300

QY 301 STSISGERRRIQKOLLADVAQALDIPAGPLMGVVQYGDNPATPHNLKTHNTSREDLKTAI 360
DB 301 STSISGERRRIQKOLLADVAQALDIPAGPLMGVVQYGDNPATPHNLKTHNTSREDLKTAI 360

QY 361 EKITQRGGLSNVGRASIFVTKNPFSKANGNRSGAPNVVVVMDGWPDKVVERASRLARES 420
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QY 421 GINIPITITTEGAENEKQVVEPNEANKAVCRITNGFVSLHVQSWFGLHKTLPVKRVCD 480
DB 421 GINIPITITTEGAENEKQVVEPNEANKAVCRITNGFVSLHVQSWFGLHKTLPVKRVCD 480

QY 481 TDRLACKTCLNSADIGFVIDGSSSVGTGNFRVTLQFVTNLTKEFRI SDTDTRIGAVQYT 540
DB 481 TDRLACKTCLNSADIGFVIDGSSSVGTGNFRVTLQFVTNLTKEFRI SDTDTRIGAVQYT 540

QY 541 YEORLEFGFDKYSKPDILNAIKRVGWYSGGTSTGAALNPALEQLPKCKSPKPKRKLMI 600
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QY 601 TDCRSYDDVRI PAKAAHLKGVITVACVAAQAELEVIATPHARDHSPVDFDNLHOY 660
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QY 661 VPRIIQNICTEFNQSPRN 678
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RESULT 6

US-09-989-732-179
; Sequence 179, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyere, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C57
; CURRENT APPLICATION NUMBER: US/09/989,732
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTAKYORPPIPTTTAQ 180

Db 121 VQSLSLPRWRESFIVLESKPKKGVTPSALTYSSSKSPAAQAGETTAKYORPPIPTTTAQ 180

RESULT 8

US-09-990-442-179
: Sequence 179, Application US/09990442
: Patent No. US20020132252A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas P.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Matanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730P1C8
: CURRENT APPLICATION NUMBER: US/09/990,442
: CURRENT FILING DATE: 2001-11-14
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
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;; PRIOR APPLICATION NUMBER: 60/090862
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;; PRIOR APPLICATION NUMBER: 60/091360
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 241 PRADPGIQRDPPGAAFPQKPGVADSVLSGLVPKBELSTQSLPVSLSGDPNCKIDLSFLIDG 300
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DB 421 GINIFPTTIEGAANEKQYVVEPNFANKAVCRNTGFFSLHVQSWFGLHKTQLPLVKRVCV 480
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QY 481 TDRLACSKTCLNSADIGFVLDGSSSVCTGNFRTVLQFVTLTKPEFISDTDTTRIGAVOYT 540
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DB 481 TDRLACSKTCLNSADIGFVLDGSSSVCTGNFRTVLQFVTLTKPEFISDTDTTRIGAVOYT 540
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DB 601 TDRGRSYDDVRI PAMAHLKGVITYTAIGVAAQAQEELEVIATHPARDHSFFVDFDNLHQY 660
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QY 661 VPRIIQNICTEFNQSPRN 678
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Db 661 VPRIIQNICTEFNQSPRN 678
RESULT 10
US-09-953-604-179
; Sequence 179, Application US/09993604
; Patent No. US20020137075A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C25
; CURRENT APPLICATION NUMBER: US/09/993,604
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Indels 0; Gaps 0;
Matches 678; Conservative 0; Mismatches 0;

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Qy	61	KCPAGCQDPKHVYGTVDVYASVYCGAAVHSGVLDSGGKILVRKVGQSGYKGSYNG	120
Db	61	KCPAGCQDPKHVYGTVDVYASVYCGAAVHSGVLDSGGKILVRKVGQSGYKGSYNG	120
Qy	121	VQSLSPRWRESFIVLESKPKGGVTPSALTYSKSPAAQAGETTKAVQRPPIPTTTAQ	180

Db 121 VOSLSLPRWRSFVLESKPKRGVTPSALITYSSKSPAAGETTKAYQRPPIPGTTAQ 180
Qy 181 PVTLMQLLAVTAVATPTTLPRPSPSAASITTSIPRPSQVGHRSQRMDLWSTATTSSQNR 240
Db 181 PVTLMQLLAVTAVATPTTLPRPSPSAASITTSIPRPSQVGHRSQRMDLWSTATTSSQNR 240
Qy 241 PRADPGIORQPSGNAPOKPGADVSLGLVPEKELSTOSLSPVSGDPCNKIDLSFLIDG 300
Db 241 PRADPGIORQPSGNAPOKPGADVSLGLVPEKELSTOSLSPVSGDPCNKIDLSFLIDG 300
Qy 301 STSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATHPNLKHTNSRDLKTAI 360
Db 301 STSICKRRFRIOKOLLADVAQALDIGPAGPLMGVVQYGDNPATHPNLKHTNSRDLKTAI 360
Qy 361 EKITQSGLSNVGRAISFVTKNFTSKANGNSGAPNVVVVMDGWPDKVBEASRLARES 420
Db 361 EKITQSGLSNVGRAISFVTKNFTSKANGNSGAPNVVVVMDGWPDKVBEASRLARES 420
Qy 421 GINIFFITIEGAENKQYVVEPNFANKAVCTRTNGFYSLHVQSWFGLKHTLOPLVKRVCD 480
Db 421 GINIFFITIEGAENKQYVVEPNFANKAVCTRTNGFYSLHVQSWFGLKHTLOPLVKRVCD 480
Qy 481 TDLRACSTKCLNSADIGFVIDGSSSVGTGNFTVLQFVNTLTKEPEISDTRIGAVOYT 540
Db 481 TDLRACSTKCLNSADIGFVIDGSSSVGTGNFTVLQFVNTLTKEPEISDTRIGAVOYT 540
Qy 541 YEORLEFGDFKYSKPDILNAIKRVGYWSGGTSTGAAINFALBOLFKKSKNKRKMLILI 600
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Qy 661 VPRIIQTICFNSOPRN 678
Db 661 VPRIIQTICFNSOPRN 678

RESULT 11
US-09-990-456-179
; Sequence 179, Application US/09990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730FIC22
; CURRENT APPLICATION NUMBER: US/09/990,456

; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.7e-293; Mismatches 0; Indels 0; Gaps 0;
Matches 678; Conservative 0;

Qy 1 MRTVLTWKASVEMFLVLLVTGVHSNKTAKIKRPKFTVPQINCDVKAGKIIDPEFIV 60
Db 1 MRTVLTWKASVEMFLVLLVTGVHSNKTAKIKRPKFTVPQINCDVKAGKIIDPEFIV 60
Qy 61 KCPAGCQDPKYHYVTGTDVYASYSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
Db 61 KCPAGCQDPKYHYVTGTDVYASYSVCGAAVHSGVLDNSGGKILVRKVAQSGYKGSYNG 120
Qy 121 VQSLSPRWRESPIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPTTTAQ 180
Db 121 VQSLSPRWRESPIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYORPPIPTTTAQ 180
Qy 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHSQEMDLWSTATTYTSSQNR 240
Db 181 PVTLMQLLAVTVAVATPTTLPRPSPSAASTTISIPRQSVGHSQEMDLWSTATTYTSSQNR 240
Qy 241 PRADPGIORQDPGSGAAPQKPVGADVSLGLVPKHELSTQSLPVSIGDPNCKIDLSPIDG 300
Db 241 PRADPGIORQDPGSGAAPQKPVGADVSLGLVPKHELSTQSLPVSIGDPNCKIDLSPIDG 300
Qy 301 STSIGKRFRFRIQKOLLADVAQALDIGPAGPLMGVVOYGDNPATFNLTHTNSRDLKTAI 360
Db 301 STSIGKRFRFRIQKOLLADVAQALDIGPAGPLMGVVOYGDNPATFNLTHTNSRDLKTAI 360
Qy 361 EKITORGGLSNVGRASIFVTNPFPSKANGNSGAPNVVWVDGFWPTDKVBEASRLARES 420
Db 361 EKITORGGLSNVGRASIFVTNPFPSKANGNSGAPNVVWVDGFWPTDKVBEASRLARES 420
Qy 421 GINIFPITIEGAAENKQYVVEPNPANKAVCKTNGFYSLHVQSWFGLHKTLPVKRVC 480
Db 421 GINIFPITIEGAAENKQYVVEPNPANKAVCKTNGFYSLHVQSWFGLHKTLPVKRVC 480
Qy 481 TDLRACSKTCLNSADIGFVIDGSSVGVGNFRTVLQVTLTKBPEISDTDTTRIGAVQVT 540
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Qy 541 YEQRLEFGFDKYSSKPDILNAIKRYVYNSGGTSTGAINFALQOLPKSKPNKRKLMI 600
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Qy 601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAQBELEVIAHPARDHSFFVDFDLHQY 660
Db 601 TDGRSYDDVRIPAMAAHLKGVITYAIGVAAQAQBELEVIAHPARDHSFFVDFDLHQY 660
Qy 661 VPRITQNICTEFNSQPRN 678

Db 661 VPRIIQNICTEFSQPN 678

RESULT 12

US-09-989-721-179

Sequence 179, Application US/099897721

Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deanoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerttsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: KJavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C55

CURRENT APPLICATION NUMBER: US/09/989,721

CURRENT FILING DATE: 2001-11-19

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PRIOR FILING DATE: 1997-06-16

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153 PRIOR FILING DATE: 1998-07-02
154 PRIOR APPLICATION NUMBER: 60/091633
155 PRIOR FILING DATE: 1998-07-02
156 PRIOR APPLICATION NUMBER: 60/091978
157 PRIOR FILING DATE: 1998-07-07
158 PRIOR APPLICATION NUMBER: 60/091982
159 PRIOR FILING DATE: 1998-07-07
160 PRIOR APPLICATION NUMBER: 60/092182
161 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRTVLTAKASVEMFLVLLVTGHSNKEAKKIKRPFVTPQINCVDKAGKIIDPEFIV 60

Qy 61 KCPAGODPKYHYVGTVDYASVSCGAHVHSGVLDNSGGKILVRKVAGOSGYKGSYNG 120
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RESULT 13
US-09-992-598-179
; Sequence 179, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Pong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCES: P2730P1C20

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1 PRIOR APPLICATION NUMBER: 60/090696
2 PRIOR FILING DATE: 1998-06-25
3 PRIOR APPLICATION NUMBER: 60/090862
4 PRIOR FILING DATE: 1998-06-26
5 PRIOR APPLICATION NUMBER: 60/090863
6 PRIOR FILING DATE: 1998-06-26
7 PRIOR APPLICATION NUMBER: 60/091360
8 PRIOR FILING DATE: 1998-07-01
9 PRIOR APPLICATION NUMBER: 60/091478
10 PRIOR FILING DATE: 1998-07-02
11 PRIOR APPLICATION NUMBER: 60/091544
12 PRIOR FILING DATE: 1998-07-01
13 PRIOR APPLICATION NUMBER: 60/091519
14 PRIOR FILING DATE: 1998-07-02
15 PRIOR APPLICATION NUMBER: 60/091626
16 PRIOR FILING DATE: 1998-07-02
17 PRIOR APPLICATION NUMBER: 60/091633
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19 PRIOR APPLICATION NUMBER: 60/091978
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22 PRIOR FILING DATE: 1998-07-07
23 PRIOR APPLICATION NUMBER: 60/092182
24 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.7e-293;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRTVLTWKAASVTEMLVLLVTVGHSNKEAKTKIKRPKFTVPQINCVDKAGKIIDPEFIV 60
Db 1 MRTVLTWKAASVTEMLVLLVTVGHSNKEAKTKIKRPKFTVPQINCVDKAGKIIDPEFIV 60
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Qy 181 PVTLMQLLVAVATPTTLPRPSPASATTSIPRQSVGHRSEMDLWSTATTYSSQNR 240
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Qy 241 PRADPGIQRDPSCGAARQKPVGADVSLGLVPKEELSTQSLPVSGLGPNCKIDLSFLIDG 300
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Qy 301 STSIGKRRFRIQKOLLADVAQALDIGPAGPLMGVVOYQYGDNPATFNLKTHNTRDLKTAL 360
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Db 361 EKITRGGLSNVGAISFVTKNPFKANGVSGAPNVVWVDCGWPTDKVEASRLARES 420
Qy 421 GINIFPFTIEGAENRQYVVEFPFANKAVCRITNGFYSLHVQSMFGLKTLQPLVKEVCD 480
Db 421 GINIFPFTIEGAENRQYVVEFPFANKAVCRITNGFYSLHVQSMFGLKTLQPLVKEVCD 480
Qy 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVTLQFVTNLTKFEISDTRIGAVOYT 540
Db 481 TDRLACSKTCLNSADIGFVIDGSSSVGTGNFRVTLQFVTNLTKFEISDTRIGAVOYT 540
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Db 661 VPRIIQICTEFSQREN 678
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; Sequence 179, Application US/09989293A
; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJ, Javin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3502; DB 9; Length 678;
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Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC61
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Db 601 TDGHSYDDVIRIPANAHLKGVITYAIGVAAQAQBELEVIATHPARDHSPFVDEPNLHOY 660

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OM protein - protein search, using sw model

Run on: May 27, 2004, 16:41:07 ; Search time 22 Seconds
(without alignments)
1604.708 Million cell updates/sec

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Perfect score: 3502

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Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1139	32.5	547	1 COCH_CHICK	O42163 gallus gall
2	1129.5	32.3	550	1 COCH_HUMAN	O43405 homo sapien
3	1113	31.8	552	1 COCH_MOUSE	Q62507 mus musculus
4	554	15.8	3124	1 CA1C_CHICK	P13944 gallus gall
5	552	15.5	3119	1 CA1C_MOUSE	Q60847 mus musculus
6	543.5	15.5	3063	1 CA1C_HUMAN	Q99715 homo sapien
7	504.5	14.4	3137	1 CA36_CHICK	P15989 gallus gall
8	501.5	14.3	496	1 CMAA_HUMAN	P21941 homo sapien
9	490	14.0	493	1 CMAA_CHICK	P05099 gallus gall
10	490	14.0	500	1 CMAA_MOUSE	P51942 mus musculus
11	471.5	13.5	3176	1 CA36_HUMAN	P12111 homo sapien
12	431.5	12.3	619	1 MTN4_HUMAN	O95460 homo sapien
13	412.5	11.8	624	1 MTN4_MOUSE	O89029 mus musculus
14	358.5	10.2	956	1 MTN2_HUMAN	O00339 homo sapien
15	337.5	9.6	956	1 MTN2_MOUSE	O08746 mus musculus
16	331	9.5	1888	1 CA1E_CHICK	P32018 gallus gall
17	329.5	9.4	2944	1 CA17_HUMAN	Q02388 homo sapien
18	280.5	8.0	929	1 CA1C_NOTVI	Q91145 notophthalm
19	279	8.0	3767	1 MUD3_CABEL	P34576 caenorhabdi
20	266	7.6	2813	1 VWF_HUMAN	O34275 homo sapien
21	262	7.5	481	1 MTN3_MOUSE	O05701 mus musculus
22	252.5	7.2	1019	1 CA16_CHICK	P20785 gallus gall
23	251	7.2	486	1 MTN3_HUMAN	O15232 homo sapien
24	248.5	7.1	452	1 MTN3_CHICK	O42401 gallus gall
25	248.5	7.1	2482	1 VWF_FIG	Q28833 sus scrofa
26	248	7.1	1329	1 KFL10_HUMAN	Q9P218 homo sapien
27	241.5	6.9	2813	1 VWF_CANFA	Q28295 canis famil
28	231	6.6	1152	1 ITAM_HUMAN	P11215 homo sapien
29	229	6.5	1153	1 ITAM_MOUSE	P05555 mus musculus
30	228	6.5	1028	1 CA16_HUMAN	P12109 homo sapien
31	228	6.5	1163	1 ITAX_HUMAN	P20702 homo sapien
32	226.5	6.5	1025	1 CA16_MOUSE	Q04857 mus musculus
33	219.5	6.3	1162	1 ITAD_HUMAN	Q13349 homo sapien

34	211.5	6.0	639	1 CA1C_RABIT	Q28902 oryctolagus
35	209.5	6.0	1022	1 CA26_CHICK	P15988 gallus gall
36	207.5	5.9	1170	1 ITAL_HUMAN	P20701 homo sapien
37	205	5.9	1029	1 CA26_MOUSE	Q02788 mus musculus
38	203.5	5.8	1180	1 ITAL_RAT	P18614 rattus norv
39	200	5.7	1019	1 CA26_HUMAN	P12110 homo sapien
40	195	5.6	1163	1 ITAL_MOUSE	P24063 mus musculus
41	193	5.5	1151	1 ITAL_HUMAN	P56199 homo sapien
42	192.5	5.5	1189	1 ITAH_HUMAN	Q9ukx5 homo sapien
43	188.5	5.4	285	1 ITAL_CHICK	Q90615 gallus gall
44	187.5	5.4	1170	1 ITA2_BOVIN	P53710 bos taurus
45	182.5	5.2	1181	1 ITA2_HUMAN	P17301 homo sapien

ALIGNMENTS

RESULT 1

ID	COCH_CHICK	STANDARD;	PRT;	547 AA.
AC	O42163;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Cochlin precursor (COCH-SB2).			
GN	COCH OR COCHSB2.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.			
RC	STRAIN=White leghorn; TISSUE=Basilar papilla;			
RX	MEDLINE=98409669; PubMed=9736748;			
RA	Heller S., Sheane C.A., Javed Z., Hudspeth A.J.;			
RT	"Molecular markers for cell types of the inner ear and candidate genes for hearing disorders."			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:11400-11405(1998).			
CC	- - SUBCELLULAR LOCATION: Secreted (Potential).			
CC	- - TISSUE SPECIFICITY: Expressed in inner ear structures; the spindle-shaped cells of the basilar papilla. Weaker expression found in the inferior and superior fibrocartilaginous plates and skeletal muscle.			
CC	- - DEVELOPMENTAL STAGE: Specifically expressed at the late developmental stages in the cochlea.			
CC	- - SIMILARITY: Contains 1 LCCL domain.			
CC	- - SIMILARITY: Contains 2 VWF domains.			
CC	- - DATABASE: NAME=Protein Spotlight;			
CC	NOTE=Issue 4 of November 2000;			
CC	WWW="http://www.expasy.org/spotlight/articles/spotlt004.html".			

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EMBL; AF012252; AAC62253.1; -
HSSP; P11215; 1JLM.
DR InterPro; IPR004043; LCCL dom.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00092; vwa; 2.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00327; VWA; 2.
DR PROSITE; PS50820; LCCL; 1.
DR PROSITE; PS50234; VWF; 2.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
POTENTIAL.

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FT CHAIN 20 547 COCHLIN.
FT DOMAIN 24 117 LCCL.
FT DOMAIN 162 347 WFPA 1.
FT DOMAIN 364 534 WFPA 2.
FT DISULFID 30 46 BY SIMILARITY.
FT DISULFID 50 70 BY SIMILARITY.
FT CARBOHYD 218 218 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 547 AA; 59426 MW; 172724242641DF88 CRC64;

Query Match 32.5%; Score 1139; DB 1; Length 547;
Best Local Similarity 37.3%; Pred. No. 2.8e-67;
Matches 229; Conservative 104; Mismatches 165; Indels 116; Gaps 5;

Qy 60 VKPAGCDDPKYHYGTDVYASVSGCAAVHSGVLDNSGKILVRKVGAGSGYGSYN 119
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 44 VLPFANCPWQFYVFGDIYASVSGCAAHRGVITNAGGAVRQVLPQENYPAVHAN 103
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 120 GVQSLSPRRRESFIVLESKPKGVTPYPSALTYSSKSPRAQAQETTKAVQRPPICTYA 179
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 104 GIOSQVLSRWASSFSV-----TPGTNN 125
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 180 QPVTLMQLLAVTAVATPTTLPRPSPAASSTISIPRQSVGHRSGQEMDLKSTATYTSSQN 239
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 126 ---LALRAGVRSVATRAPAT-----142
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 240 RPRADPGIORQDPGSAAPQKPGVADVSLGLVPKEELSTQSLPVSGLDPPNCKIDLSFLID 299
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 143 -----GKRPKTKLEKA-----GNCKCKADIAFLID 168
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 300 GSTSIGKRRPRIQKLLADVAQALDIPAGPLMGVQVQGNPDATHFNLKTHNSRDLKTA 359
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 169 GSYNIGQRRENLQNFVGVKAVMLGIGTEGPHGVQVQASEHPKIEFYLKNTFAKRYLFA 228
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 360 IEXTORGGISNVCRAISFVTKNPFSGKANGRCAPNVVVMDGWPDKVVERASLRAR 419
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 229 IKELGFGGNSNTGKALKHAQKPFSENGARKGIPKILVFLDGNFSDDEERAGIVARE 288
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 420 SGINIPITTEGAENEKQYVVEFNFAKVCRTNGFYSLHVQVWFLGHLTKLOPLVRVC 479
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 289 FGYNVFIIVSAKPTTEELGMVQDIFGDKAVCRNNGFFSYQMPSPFGTKVKVQLVKLC 348
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 480 DTRLACSKTCLNSADIGFVIDGSSSVGTGFRVTLQFVNLTKPEISDTDTIGAVOY 539
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 349 SHEQMLCKTCTYNSWNLGFLIDGSSVGSNFRMLFEFISNVAKAFRISDGSKIATVQF 408
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 540 TYEORLEPGDKYSSKPDILNAIKRVGVWSGTGTGAALNPALEQLFKSKPKPKR-LMI 598
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 409 TYDQTEFSFYDYTKKSKVLSAIRNRYMSGGTATGDAISFTTRNVFGPVNDGANKNPLV 469
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 599 LITDGRSYDDVRIPAMAHLKGVITYAIGVAAQAQEBLEVIATHPARDHSFFVDFDNLH 658
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 469 ILTDGQSYDDVRGPAVAAQKAGITVPSGVGAVAPLDLKLKOWASPRESHPTFTTREFGLE 528
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Qy 659 QYVPRITONICTEP 672
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :
Db 529 QWVPDVIRGICKDF 542
| | | | | : : : | | | | | : : : | | | | | : : : | | | | | : : :

RESULT 2
COCH HUMAN STANDARD; PRT; 550 AA.
AC 043405;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
Db Cochlin precursor (COCH-5B2) (UNQ257/PRO294).
GN COCH OR COCH5B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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```

RC TISSUE=Cochlea;
RA MEDLINE=98110569; PubMed=9441737;
RA Robertson N.G., Skvorak A.B., Yin Y., Weremowicz S., Johnson K.R.,
RA Kovatch K.A., Battey J.F., Bieber F.R., Morton C.C.;
RT "Mapping and characterization of a novel cochlear gene in human and in
RL mouse: a positional candidate gene for a deafness disorder, DFNA9.";
RN Genomics 46:345-354 (1997).
RP SEQUENCE FROM N.A.
RP MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Liang L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandelin R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270 (2003).
RN [3]
RP N-GLYCOSYLATION, SUBCELLULAR LOCATION, AND PROTEOLYTIC PROCESSING.
RA MEDLINE=22727166; PubMed=12843317;
RA Robertson N.G., Hanaker S.A., Patriub V., Aster J.C., Morton C.C.;
RT "Subcellular localization, secretion, and post-translational
RT processing of normal cochlin, and of mutants causing the
RT sensorineural deafness and vestibular disorder, DFNA9.";
RL J. Med. Genet. 40:479-486 (2003).
RN [4]
RP STRUCTURE BY NMR OF 27-126.
RA MEDLINE=21458424; PubMed=11574466;
RA Liepinsh E., Trexler M., Kaikkonen A., Weigelt J., Banyai L.,
RA Pathy L., Otting G.;
RT "NMR structure of the LCCL domain and implications for DFNA9 deafness
RL disorder.";
RL EMBO J. 20:5347-5353 (2001).
RN [5]
RP VARIANTS DFNA9 GLY-66; GLU-88 AND ARG-117.
RA MEDLINE=99021390; PubMed=9806553;
RA Robertson N.G., Lu L., Heller S., Merchant S.N., Eavey R.D.,
RA McKenna M., Nadol J.B. Jr., Miyamoto R.T., Linthicum F.H. Jr.,
RA Neto J.F.L., Hudspeth A.J., Seidman C.E., Morton C.C., Seidman J.G.;
RT "Mutations in a novel cochlear gene cause DFNA9, a human nonsyndromic
RT deafness with vestibular dysfunction.";
RL Nat. Genet. 20:299-303 (1998).
RN [6]
RP VARIANT DFNA9 SER-51.
RA MEDLINE=99135917; PubMed=9931344;
RA de Kok Y.J.M., Bom S.J.H., Brunt T.M., Kemperman M.H.,
RA van Beusekom E., van der Velde-Visser S.D., Robertson N.G.,
RA Morton C.C., Huygen P.L.M., Verhagen W.I.M., Brunner H.G.,
RA Cremers C.W.R.J., Cremers F.P.M.;
RT "A pro51-to-ser mutation in the COCH gene is associated with late
RT onset autosomal dominant progressive sensorineural hearing loss with
RL vestibular defects.";
RL Hum. Mol. Genet. 8:361-366 (1999).
RN [7]
RP VARIANT DFNA9 ASN-109.
RA MEDLINE=21193177; PubMed=11295836;
RA Kamarinos M., McGill J., Lynch M., Dahl H.-H.M.;
RT "Identification of a novel COCH mutation, I109N, highlights the
RL similar clinical features observed in DFNA9 families.";
RN Hum. Mutat. 17:351-351 (2001).
RN [8]
RP ERRATUM.
RA Kamarinos M., McGill J., Lynch M., Dahl H.-H.M.;
RL Hum. Mutat. 18:547-548 (2001).
RN [9]
RP VARIANT DFNA9 THR-119.
RA MEDLINE=22873884; PubMed=14512963;
RP

```


[illegible]

continues to be expressed in several tissues, even after birth.
 The long NCI isoforms, X11A-1 and X11B-1, peak in 15-day old embryos and decrease in 17-day old ones. The expression of the short NCI form X11B-2 remains constant throughout late stages of embryonic development (ED15 and ED17).
 -1- PWM: The triple-helical tail is stabilized by disulfide bonds at each end (By similarity).
 -1- PWM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains (By similarity).
 -1- PWM: O-glycosylation of isoform X11A-2; glycosaminoglycan of chondroitin-sulfate type (By similarity).
 -1- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH INTERRUPTED HELICES (FACIT) FAMILY.
 -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 -1- SIMILARITY: Contains 4 VWFA domains.
 -1- SIMILARITY: Contains 18 fibronectin type III domains.

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 EMBL; U25652; AAA9719.1; ALT_SEQ.
 DR EMBL; U57095; AAB07047.1; .
 DR HSP; P02751; 1FWA.
 DR MGD; MGI:88448; Coll2a1.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008957; FN III-like.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003129; TSPN.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF01391; Collagen; 5.
 DR Pfam; PF00041; fn3; 18.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PF00092; vwa; 4.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00060; FN3; 18.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00327; VWA; 4.
 DR PROSITE; PS0234; VWFA; 4.
 DR Cell adhesion; Collagen; Connective tissue; Repeat; Hydroxylation;
 KW Extracellular matrix; Signal; Glycoprotein; Alternative splicing.
 FT SIGNAL 1 24
 FT CHAIN 25 3119
 FT COLLAGEN ALPHA 1(XII) CHAIN.
 FT FIBRONECTIN TYPE-III 1.
 FT VWFA 1.
 FT FIBRONECTIN TYPE-III 2.
 FT VWFA 2.
 FT FIBRONECTIN TYPE-III 3.
 FT FIBRONECTIN TYPE-III 4.
 FT FIBRONECTIN TYPE-III 5.
 FT FIBRONECTIN TYPE-III 6.
 FT FIBRONECTIN TYPE-III 7.
 FT FIBRONECTIN TYPE-III 8.
 FT VWFA 3.
 FT FIBRONECTIN TYPE-III 9.
 FT FIBRONECTIN TYPE-III 10.
 FT FIBRONECTIN TYPE-III 11.
 FT FIBRONECTIN TYPE-III 12.
 FT FIBRONECTIN TYPE-III 13.
 FT FIBRONECTIN TYPE-III 14.
 FT FIBRONECTIN TYPE-III 15.
 FT FIBRONECTIN TYPE-III 16.
 FT FIBRONECTIN TYPE-III 17.
 FT FIBRONECTIN TYPE-III 18.
 FT VWFA 4.
 FT TSP N-TERMINAL.
 FT NON-HELICAL REGION (NC3).
 FT TRIPLE-HELICAL REGION

(COL2) WITH 1 IMPERFECTION.
 NON-HELICAL REGION (NC2).
 TRIPLE-HELICAL REGION
 (COL1) WITH 2 IMPERFECTIONS.
 NON-HELICAL REGION (NC1).
 CELL ATTACHMENT SITE (POTENTIAL).
 CELL ATTACHMENT SITE (POTENTIAL).
 CELL ATTACHMENT SITE (POTENTIAL).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 HYDROXYLATION (BY SIMILARITY).
 POLY-THR.
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 O-LINKED (XYL. . .) (CHONDROITIN SULFATE) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 Missing (in isoform X11B-1 and isoform X11B-2).
 /FTID=VSP 001150.
 BPI -> GSG (in isoform X11A-2 and isoform X11B-2).
 /FTID=VSP 001151.
 Missing (in isoform X11A-2 and isoform X11B-2).
 /FTID=VSP 001152.
 /FTID=VSP 001152.
 9B1F999C86AB3251 CRC64;
 SQ SEQUENCE 3119 AA; 340239 MM; 9B1F999C86AB3251 CRC64;
 Query Match 15.8%; Score 552; DB 1; Length 3119;
 Best Local Similarity 27.5%; Pred. No. 1.1e-27;
 Matches 174; Conservative 77; Mismatches 209; Indels 172; Gaps 16;
 QY 168 AYQRP--PIPG--TTAQPTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPSQVGHRS 223
 Db 44 SWERPVDPIVGRITVDPTDGTKEFTLAASSTETL-----LSDLIPETQYV--- 91
 QY 224 QEMDLNSTATYTSQNRPRADP-----GIQODPSGAAPKPEVGADVSLGLVPKBLSTQ 278
 Db 92 -----VTTTSNVEESVPVIGQLTIQGGTPKGEKPKTEIQ----- 131
 QY 279 SLEPVSIGDPNCKI-----DLSELDIGSTSIGRRRRIQKLLADVAQALDIPAGPLMGV 334
 Db 132 -----KCSVSAWTDLVFLVDGWSVGRNNFKYILDFIVALVSADFGEKTRGV 181
 QY 335 VOYGDNPATNLTHTNSRDLKTAIEKIQRGGLSNVGRALSFVTKNPFPSKANGRSGA 394
 Db 182 VOYGSSTRTETFLNQYRERDLAAVKKIPYKGGNTMTGDAIDYLVKNTFTTESAGSRAP 241
 QY 395 PNVVVVMDGWPTDKVREASRLRESGINIPITIEGA-AENEKQVYVREP-----NPA 447
 Db 242 PKVGIIITDGKSQDEVEIPARELRNIGVEVSGINRAADAKELKQIASTPSLNHNVAN 301
 QY 448 -----KAVC----- 453
 Db 302 FDAIVDIQNEIISQVSGVDEQLGELVSGVEVIEPPSNLVVLTSLSSKYIRLSWDPSPSAV 361

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QY 454 NGF-----YSLVQSWFGL-----HK 469
Db 362 TGYKILLTPMAGSRHSLSVGPQTTLINVRDLTADTEYQISFAMKGLTSSEPTSMYK 421
QY 470 T---LQPLVKRVCVDTDLACSKTCLNSADIGFVLDGSSVGTGNFRTVLOFVNLTKEFE 526
Db 422 TQKPTQMKVQV-----ECSRGVDIKADIVFLVDSYSIGTANFVKVRAFLVLAKEFE 475
QY 527 ISPTDTRIGAVQVYTYEQRLEPFGDKYSSKPDILNAIKRVGVWGSCTGTGAANPALBOLF 586
Db 476 ISPNRVQISLVQVSRDPHTFTLKEFNRVEDIINKAINTFPYRGSGTNTGKAMTYVREKIF 535
QY 587 ----KSKPNRKMLMLITDGRSDVDVRIPMAHAHLKGVITYATGVAVAAQEELEVIATHP 643
Db 536 VPKRGSNSVPKVMILITDGESSDAFRDPAKLENSDVEIPAVGVKDDAVRSELEIASPP 595
QY 644 ARDSFPPVDFDNLHGVQVPRILIONICTEFNSQ 675
Db 596 AETHVTFVEDFDAPQISFVLVTQSCILRIQOE 627

RESULT 6
CAIC_HUMAN
ID CAIC_HUMAN STANDARD; PRT; 3063 AA.
AC Q99715; Q99716;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Collagen alpha 1(XII) chain precursor.
GN COL12A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
RX MEDLINE=97288521; PubMed=9143499;
RA Gerecke D.R., Olson P.F., Koch M., Knoll J.H.M., Taylor R.,
RA Hudson D.L., Champlaud M.-F., Olsen B.R., Burgeson R.E.;
RT "Complete primary structure of two splice variants of collagen XII,
RT and assignment of alpha 1(XII) collagen (COL12A1), alpha 1(XI)
RT collagen (COL9A1), and alpha 1(XIX) collagen (COL19A1) to human
RT chromosome 6q12-q13."
RL Genomics 41:236-242(1997).
CC -!- FUNCTION: Type XII collagen interacts with type I collagen-
CC containing fibrils, the COL1 domain could be associated with the
CC surface of the fibrils, and the COL2 and NC3 domains may be
CC localized in the pericellular matrix (By similarity).
CC -!- SUBUNIT: Trimer of identical chains each containing 190 kDa of
CC nontriple-helical sequences.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=The final tissue form of collagen XII may contain
CC homotrimers of either isoform long or isoform short or any
CC combination of isoform long and isoform short;
CC Name=Long;
CC IsoId=Q99715-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q99715-2; Sequence=VSP_001149;
CC -!- TISSUE SPECIFICITY: Found in collagen I-containing tissues: both
CC short and long isoforms appear in amnion, chorion, skeletal
CC muscle, small intestine, and in cell culture of dermal
CC fibroblasts, keratinocytes and endothelial cells. Only the short
CC isoform is found in lung, placenta, kidney and a squamous cell
CC carcinoma cell line.
CC -!- PTM: The triple-helical tail is stabilized by disulfide bonds at
CC each end (By similarity).
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains (By
CC similarity).
CC -!- PTM: O-glycosylation of isoform long; glycosaminoglycan of
CC chondroitin-sulfate type (By similarity).
CC -!- SIMILARITY: BELONGS TO THE FIBRIL-ASSOCIATED COLLAGENS WITH

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CC INTERRUPTED HELICES (FACIT) FAMILY.
CC -!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -!- SIMILARITY: Contains 4 VWFA domains.
CC -!- SIMILARITY: Contains 18 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U73778; AAC51244.1; --
CC DR EMBL: U73779; AAD40483.1; --
CC DR HSP; P02751; ITTF.
CC DR Genew; HGNC:2188; COL12A1.
CC DR MIM; 120320; --
CC DR GO; GO:0005595; C:collagen type XII; TAS.
CC DR GO; GO:0001501; P:skeletal development; TAS.
CC DR InterPro; IPR008160; Collagen.
CC DR InterPro; IPR008957; FN III-like.
CC DR InterPro; IPR003961; FN III.
CC DR InterPro; IPR003129; TSPN.
CC DR InterPro; IPR002035; VWFA_A.
CC DR Pfam; PF01391; Collagen; 4.
CC DR Pfam; PF00041; fn3; 18.
CC DR Pfam; PF02210; TSPN; 1.
CC DR Pfam; PF00092; vwa; 4.
CC DR PRINTS; PR00453; VWFADOMAIN.
CC DR SMART; SM00060; FN3; 16.
CC DR SMART; SM00210; TSPN; 1.
CC DR SMART; SM00327; VWA; 4.
CC DR PROSITE; PS0234; VWFA; 4.
CC DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
CC Cell adhesion; Collagen; Signal; Glycoprotein; Alternative splicing.
CC POTENTIAL.
CC SIGNAL 1 24
CC CHAIN 25 3063
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FT MOD_RES 2959 2959 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 2965 2965 HYDROXYLATION (BY SIMILARITY).
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FT MOD_RES 3000 3000 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3003 3003 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3014 3014 HYDROXYLATION (BY SIMILARITY).
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FT MOD_RES 3026 3026 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 3029 3029 HYDROXYLATION (BY SIMILARITY).
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FT CARBOHYD 2679 2679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 25 1188 Missing (in isoform Short).
FT SEQUENCE 3063 AA; 333189 MM; 75FEA78FABE48293 CRC64;

Query Match 15.5%; Score 543.5; DB 1; Length 3063;
Best Local Similarity 27.7%; Pred. No. 4e-27;
Matches 172; Conservative 76; Mismatches 207; Indels 165; Gaps 16;

Qy 179 AQPVTLMQLLAVTAVATPTTLPRSPS-----AASSTTS-----IPRQSVGHRSEQMD 227
Db 46 AEPVDPVIGYRITV---DPTT---DPTKEFTLSATTTLLSELVPEYEV----- 91
Qy 228 LWSATYTTSSQNRPADFCIQDPSGAAFOKPGVADYSLGLVPKHELSTQSLSPVSLGD 287
Db 92 -----VTITSYDEVESVPIQGLTITQGSSTKPV-----EKKPGKTEI 130
Qy 288 PNCKI-----DLSFLDGTSGIKRRFRIQKLLADVAQALDIPAGPLMGVQYQDNPAT 343
Db 131 QKCSVSAMTDLVFLVDGWSVGRNNPKYILDFIALVSAFDLGEKTRVGQVQYSSDRT 190
Qy 344 HFNLTHTNSRLKTAIKTQKGLSNVGRSAISFVTRNFFSKANGNRSGAPNVVVVMD 403
Db 191 EFNLYQYQORDELLAAIKKIPYKGGNTWTGDAIDYLVKNTFTESAGARVGPVKVAILTD 250
Qy 404 GWPTDKVEARSLARESGINFFPIEGA-AENEKQYVVEP-----NEAN----- 447
Db 251 GKSQDEVEIPARELRNVGVVEFSLGKAADAKELQIASFTPSLNHVFNVPANFPAIDVION 310
Qy 448 ---KAVCR-----TNGF----- 456
Db 311 ELISQCSGVDEQLGELVSGBEVPEPPSMLIAEVSSKYVKNWNPSPVTVGYKVILTP 370
Qy 457 -----YSLHVQSWFG-----LHKTQLPLVKRY 478
Db 371 MTAGSRQHALSVGPQTTLTVRDLSDADTEYQISVSAAMKQWTSSEPTSIEMKT-QPMKVQV 429
Qy 479 CDTDLASCKTCLNSADIGFVIDGSSVGTGFRVTLQPVNLTKEFESIDTDTTRIGAVQ 538
Db 430 -----ECSRGVDIIRADIIVFLVDGYSIGIANFVKVRAFLVFLVKSFEISPNRVQISLVQ 483
Qy 539 YTEQRLRPGFKYSKPDILNAIKRVGWSGCTSGAINFALRGLP---KKSKPNKKK 595
Db 484 YSRDPHTETLKKTKVEDIIEALINTPYRGSGTWTGKATVYREKIFVPSKGSNSVPK 543
Qy 596 LMLITDGRSYDDVRIPAMAHLKGVITYTAIGVANAQAELEVIATHPARDHSFFVDEPD 655
Db 544 VMLITDGRSDAPRDPALIKRNSDVEIFAVGVKDAVRSELEALASPPAETHVFTVEDFD 603
Qy 656 NLHQVVPRIQNICTEFNSQ 675
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Db 604 AFQRISFELTQSICLRIRQE 623
RESULT 7
CA36 CHICK
ID CA36 CHICK STANDARD; PRT; 3137 AA.
AC P15989;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Collagen alpha 3(VI) chain precursor.
GN COL6A3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RP SEQUENCE OF 1-853 FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=91035630; PubMed=1977751;
RA Doliana R., Bonaldo P., Colombatti A.;
RT "Multiple forms of chicken alpha 3(VI) collagen chain generated by
RT alternative splicing in type A repeated domains.";
RL Biochemistry 29:1245-1254(1990).
RN [2]
RP SEQUENCE OF 224-2871 FROM N.A.
RX MEDLINE=90212613; PubMed=2322559;
RA Bonaldo P., Russo V., Bucciotti F., Doliana R., Colombatti A.;
RT "The carboxyl terminus of the chicken alpha 3 chain of collagen VI is
RT a unique mosaic structure with glycoprotein Ib-like, fibronectin type
RT III, and Kunitz modules.";
RL J. Biol. Chem. 264:20235-20239(1989).
CC -!- FUNCTION: Collagen VI acts as a cell-binding protein.
CC -!- SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
CC alpha 2(VI), and alpha 3(VI).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=At least 2 isoforms are produced;
CC Name=1;
CC IsoId=PI5989-1; Sequence=Displayed;
CC -!- PTM: Prolines at the third position of the tripeptide repeating
CC unit (G-X-Y) are hydroxylated in some or all of the chains.
CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- SIMILARITY: Contains 12 WFEA domains.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M24282; AAA03201.1; -
CC PIR; A37797; A37797.
CC HSP; P12111; 2KMT.
CC InterPro; IPR008161; Clg helix.
CC InterPro; IPR008160; Collagen.
CC InterPro; IPR003961; FN III.
CC InterPro; IPR002223; Kunitz_BPTI.
CC InterPro; IPR002035; VWF A.
CC Pfam; PF01391; Collagen; 6.
CC Pfam; PF00041; fn3; 1.
CC Pfam; PF00014; Kunitz_BPTI; 1.
CC DR
```

```
DR Pfam; PF00092; vwa; 11.
DR PRINTS; PR00759; BASICPTASE.
DR PRINTS; PR00453; VWFADOMAIN.
DR ProDom; PD000007; Cig helix; 1.
DR ProDom; PD000222; Kunitz_BPTI; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00131; KU; 1.
DR SMART; SM00327; VWA; 12.
DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
DR PROSITE; PS0234; VWFV; 12.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Serine protease inhibitor; Collagen;
KW Signal; Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 3137
FT DOMAIN 26 2042
FT DOMAIN 2043 2379
FT DOMAIN 2380 3137
FT DOMAIN 38 212
FT DOMAIN 241 418
FT DOMAIN 444 623
FT DOMAIN 644 817
FT DOMAIN 842 1014
FT DOMAIN 1035 1207
FT DOMAIN 1239 1410
FT DOMAIN 1441 1621
FT DOMAIN 1641 1814
FT DOMAIN 1840 2029
FT DOMAIN 2407 2587
FT DOMAIN 2625 2821
FT DOMAIN 2945 3043
FT DOMAIN 3068 3137
FT SITE 2166 2172
FT SITE 2254 2259
FT SITE 2308 2309
FT SITE 2045 2047
FT SITE 2153 2155
FT SITE 2159 2161
FT ACT SITE 3082 3083
FT DISULFID 3072 3122
FT DISULFID 3081 3105
FT DISULFID 3097 3118
FT CARBOHYD 201 201
FT CARBOHYD 2084 2084
FT CARBOHYD 2436 2436
FT CARBOHYD 2563 2563
FT CARBOHYD 2581 2581
FT CARBOHYD 2683 2683
FT CARBOHYD 2867 2867
SQ SEQUENCE 3137 AA; ECB428578B536357 CRC64;

Query Match 14.4%; Score 504.5; DB 1; Length 3137;
Best Local Similarity 30.7%; Pred. No. 1.5e-24;
Matches 121; Conservative 87; Mismatches 155; Indels 31; Gaps 8;

QY 293 DLSFLDSTSTIGKRRFRIQKLLADVAQALDIDGAPGLMGVVGNDPAPNFKLTKTN 352
DB 38 DIIFLVDSSWIGKEHFQVREFLYDVVKALDVGGNDFRPAIVQSGNPHTEFQINTYPS 97

QY 353 SRLKTAIEKITORGLSNVGRALSFVTNPFPSKANGNR--GAPNVVVVMDGHTDKV 410
DB 98 NQDVLSHIANPMPYMGSGSKTGKLEYLIENHLTKAAGSRAGSEGVQVIVLTDGQSQDDV 157

QY 411 EEASRLAREGINPFTIIEGAENEKQYVVEPNFANKVCTNGTFYSLHFVQSWPGLHKT 470
DB 158 ALPSSVLKSAHVNMIAGVQDAVEGELKEIASRPEDT-----HLFNLNFTALHGI 208

QY 471 LQPLVK--RVCTDRLACKS-----TCLNGADIGFVIDGSSVGTGNFRTVLOFVNLT 522
DB 209 VGDVLASVRTSWTPEQAKGLVKDITQAQESADLIFLDGSDNIGSVNFPQAIRDFLVNLI 268

QY 523 KEFEISDITDTRIGAVQVYTYEQRLEFGFDKYSKPDILNAIKRVGYNSG-GTSTGAANFPA 581
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Db 269 ESLRVGAQQIHIGVVQVSDQRTBFALNSYSTKADVLDAVXALSFRGKEANTGALETV 328
QY 582 LEQLFKKSKPNK-----RKLMLITDGRSYDDVRIPANMAHLKGVITYTAIGVMAAOBEL 636
DB 329 VENLFTQAGSGRIEAVPQILVLISGGSSDDIREGLAVKQASIFSPSIGVNLNADSABL 388
QY 637 EVIATHPARDSFFVDEFD--NLHQYVPRITONI 668
DB 389 QQIAT----DGSFAFTALDIRNLAALRELLPNI 418

RESULT 8
CAMA HUMAN
ID CAMA_HUMAN STANDARD; PRT; 496 AA.
AC P21941;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cartilage matrix protein precursor (Matrilin-1).
GN MATN1 OR CRTM OR CMP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91060568; PubMed=2246248;
RA Jenkins R.N., Osborne-Lawrence S.L., Sinclair A.K., Eddy R.L. Jr.,
RA Byers M.G., Shows T.B., Duby A.D.;
RT "Structure and chromosomal location of the human gene encoding
RT cartilage matrix protein.";
RL J. Biol. Chem. 265:19624-19631(1990).
CC -!- FUNCTION: Cartilage matrix protein is a major component of the
CC extracellular matrix of nonarticular cartilage. It binds to
CC collagen.
CC -!- SUBUNIT: Homotrimer.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 2 WVEA domains.
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M55682; AAB38702.1; -
CC EMBL; M55675; AAB38702.1; JOINED.
CC EMBL; M55676; AAB38702.1; JOINED.
CC EMBL; M55677; AAB38702.1; JOINED.
CC EMBL; M55679; AAB38702.1; JOINED.
CC EMBL; M55680; AAB38702.1; JOINED.
CC EMBL; M55681; AAB38702.1; JOINED.
CC EMBL; M55683; AAB38702.1; JOINED.
CC PIR; A37979; A37979.
CC HSSP; P05099; LAQ5.
CC Genew; HGNC:6907; MATN1.
CC MIM; 115437;
CC GO; GO:0005578; C:extracellular matrix; TAS.
CC GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
CC GO; GO:0006461; P:protein complex assembly; TAS.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR002035; VWF_A.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00092; vwa; 2.
CC PRINTS; PR00453; VWFADOMAIN.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00327; VWA; 2.
CC PROSITE; PS00022; EGF_1; FALSE_NEG.
CC PROSITE; PS01186; EGF_2; 1.
```


Goetinck P.F.;
"Structure of the gene for cartilage matrix protein, a modular protein of the extracellular matrix. Exon/intron organization, unusual splice sites, and relation to alpha chains of beta 2 integrins, von Willebrand factor, complement factors B and C2, and epidermal growth factor.";
J. Biol. Chem. 264:8126-8134 (1989).
[2]
SEQUENCE OF 78-493 FROM N.A.
MEDLINE=87092429; PubMed=3025875;
Argraives W.S., Deak F., Sparks K.J., Kiss I., Goetinck P.F.;
"Structural features of cartilage matrix protein deduced from cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 84:464-468 (1987).
[3]
STRUCTURE BY NMR OF 447-493.
MEDLINE=97406913; PubMed=9260286;
Wilttschek R., Kammerer R.A., Dames S.A., Schulthess T.,
Blommers M.J., Engel J., Alexandrescu A.T.;
"Heteronuclear NMR assignments and secondary structure of the coiled coil trimerization domain from cartilage matrix protein in oxidized and reduced forms.";
Protein Sci. 6:1734-1745 (1997).
-!- FUNCTION: Cartilage matrix protein is a major component of the extracellular matrix of nonarticular cartilage. It binds to collagen.
-!- SUBUNIT: Homotrimer.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 2 VWFA domains.

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EMBL; X12353; CAA30915.1; -.
EMBL; X12346; CAA30915.1; JOINED.
EMBL; X12347; CAA30915.1; JOINED.
EMBL; X12348; CAA30915.1; JOINED.
EMBL; X12349; CAA30915.1; JOINED.
EMBL; X12350; CAA30915.1; JOINED.
EMBL; X12351; CAA30915.1; JOINED.
EMBL; X12352; CAA30915.1; JOINED.
EMBL; M14792; AAA48695.1; -.
EMBL; M97497; AAC18872.1; -.
PIR; A33809; A33809.
PDB; 1AQ5; 11-FEB-96.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR002035; VWF_A.
Pfam; PF00008; EGF; 1.
Pfam; PF00092; vwa; 2.
PRINTS; PR00453; VWFADOMAIN.
SMART; SM00181; EGF; 1.
SMART; SM00327; VWA; 2.
PROSITE; PS00022; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50234; VWFA; 2.
EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
3D-structure.
1 23
SIGNAL
CHAIN 24 493
DOMAIN 24 220
DOMAIN 221 261
DOMAIN 262 450
DOMAIN 462 492
CARBOHYD 74 74
DISULFID 33 219
DISULFID 225 236
DISULFID 232 245
DISULFID 247 260
CARTILAGE MATRIX PROTEIN.
VWFA 1.
EGF-LIKE.
VWFA 2.
COILED COIL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

RESULT 11
CA36 HUMAN STANDARD; PRT; 3176 AA.
ID P12111; Q16501;
AC P12111; Q16501;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Collagen alpha 3(VI) chain precursor.
GN COL6A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE=Placenta;
RC MEDLINE=90151612; PubMed=1689238;
RX Chu M.-L., Zhang R.-Z., Pan T.-C., Stokes D., Conway D., Kuo H.-J.,
RA Guanville R., Mayer U., Mann K., Deutzmann R., Timpl R.;
RT "Mosaic structure of globular domains in the human type VI collagen
alpha 3 chain: similarity to von Willebrand factor, fibronectin,
RT actin, salivary proteins and aprotinin type protease inhibitors.";
RL EMBO J. 9:385-393(1990).
RN [2]
RP REVISIONS.
RA Chu M.-L.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE OF 2038-2373 FROM N.A.
RP MEDLINE=89066644; PubMed=3198591;
RX Chu M.-L., Conway D., Pan T.-C., Baldwin C., Mann K., Deutzmann R.,
RA Timpl R.;
RT "Amino acid sequence of the triple-helical domain of human collagen
type VI.";
RL J. Biol. Chem. 263:18601-18606(1988).
RN [4]
RN SEQUENCE OF 2092-2157 FROM N.A.
RP MEDLINE=88029444; PubMed=3665927;
RX Chu M.-L., Mann K., Deutzmann R., Pribula-Conway D.,
RA Hu-Chen C.-C., Bernard M.P., Timpl R.;
RT "Characterization of three constituent chains of collagen type VI by
peptide sequences and cDNA clones.";
RL Eur. J. Biochem. 168:309-317(1987).
RN [5]
RN SEQUENCE OF 2092-2151 FROM N.A.
RP TISSUE=Placenta;
RX MEDLINE=88161046; PubMed=3348212;
RA Weil D., Mattei M.-G., Passage E., van Cong N., Pribula-Conway D.,
RA Mann K., Deutzmann R., Timpl R., Chu M.-L.;
RT "Cloning and chromosomal localization of human genes encoding the
three chains of type VI collagen.";
RL Am. J. Hum. Genet. 42:435-445(1988).
RN [6]
RN SEQUENCE OF 32-236 FROM N.A., AND ALTERNATIVE SPLICING.
RP MEDLINE=93054780; PubMed=1339440;
RX Zanussi S., Dollana R., Segat D., Bonaldo P., Colombatti A.;
RA "The human type VI collagen gene, mRNA and protein variants of the
alpha 3 chain generated by alternative splicing of an additional 5-end
exon.";
RL J. Biol. Chem. 267:24082-24089(1992).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 3107-3164.
RX MEDLINE=95182468; PubMed=7533217;
RA Arnoux B., Merigau K., Saludjian P., Norris K., Bjoern S.,
RA Olsen O., Petersen L., Ducruix A.;
RT "The 1.6 A structure of Kunitz-type domain from the alpha 3 chain of
human type VI collagen.";
RL J. Mol. Biol. 246:609-617(1995).
RN [8]
RN STRUCTURE BY NMR OF 3102-3164.
RX MEDLINE=96398604; PubMed=8805527;
RA Zweckstetter M., Cziisch M., Mayer U., Chu M.-L., Zinth W., Timpl R.,

RA Holak T.A.;
RT "Structure and multiple conformations of the Kunitz-type domain from
human type VI collagen alpha3(VI) chain in solution.";
RL Structure 4:195-209(1996).
RN [9]
RN STRUCTURE BY NMR OF 3107-3164.
RX MEDLINE=97410331; PubMed=9265624;
RA Soerensen M.D., Bjoern S., Norris K., Olsen O., Petersen L.,
RA James T.L., Led J.J.;
RT "Solution structure and backbone dynamics of the human alpha3-chain
type VI collagen C-terminal Kunitz domain.";
RL Biochemistry 36:10439-10450(1997).
RN [10]
RN DISEASE.
RX MEDLINE=21987636; PubMed=11992252;
RA Demir E., Sabatelli P., Allamand V., Ferreiro A., Moghadaszadeh B.,
RA Makrelouf M., Topaloglu H., Echenne B., Merlini L., Guicheney P.;
RT "Mutations in COL6A3 cause severe and mild phenotypes of Ullrich
congenital muscular dystrophy.";
RL Am. J. Hum. Genet. 70:1446-1458(2002).
RN [11]
RN VARIANT EM GLU-1679, AND VARIANT HIS-2831.
RX MEDLINE=98204804; PubMed=95336084;
RA Pan T.-C., Zhang R.-Z., Pericak-Vance M.A., Tandan R., Fries T.,
RA Stajich J.M., Viles K., Vance J.M., Chu M.-L., Speer M.C.;
RT "Missense mutation in a von Willebrand factor type A domain of the
alpha 3(VI) collagen gene (COL6A3) in a family with Bethlem
myopathy.";
RL Hum. Mol. Genet. 7:807-812(1998).
CC - FUNCTION: Collagen VI acts as a cell-binding protein.
CC - SUBUNIT: Trimers composed of three different chains: alpha 1(VI),
CC alpha 2(VI), and alpha 3(VI).
CC - ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=PI2111-1; Sequence=Displayed;
CC Name=2;
CC IsoId=PI2111-2; Sequence=VSP 001172;
CC - PTM: Prolines at the third position of the tripeptide repeating
unit (G-X-Y) are hydroxylated in some or all of the chains.
CC - DISEASE: Defects in COL6A3 are a cause of Bethlem myopathy (BM)
[MIM:158810]. BM is a rare autosomal dominant proximal myopathy
characterized by early childhood onset (complete penetrance by the
age of 5) and joint contractures most frequently affecting the
elbows and ankles.
CC - DISEASE: Defects in COL6A3 are a cause of Ullrich congenital
muscular dystrophy (UCMD) [MIM:254090]; also known as Ullrich
scleroatonic muscular dystrophy. UCMD is an autosomal recessive
congenital myopathy characterized by muscle weakness and multiple
joint contractures, generally noted at birth or early infancy. The
clinical course is more severe than in Bethlem myopathy.
CC - SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
CC - SIMILARITY: Contains 1 fibronectin type III domain.
CC - SIMILARITY: Contains 12 VWFA domains.

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or send an email to license@isb-sib.ch).

CC EMBL; X52022; CAA36367.1; -
DR EMBL; X06196; CAA29557.1; -
DR EMBL; M20778; -; NOT ANNOTATED_CDS.
DR EMBL; M27449; AAB52057.1; -
DR EMBL; SA9432; AAB24261.1; -
DR PIR; A59140; CGRUJA.
DR PDB; 1KNT; 01-NOV-94.
DR PDB; 2KNT; 15-MAY-97.
DR PDB; 1KUN; 12-NOV-97.
DR PDB; 1KTH; 28-AUG-02.

Event=Alternative splicing; Named isoforms=2;
 Comment=Additional isoforms seem to exist;
 Name=1;
 IsoId=095460-1; Sequence=Displayed;
 Name=2;
 IsoId=095460-2; Sequence=VSP 001400;
 TISSUE SPECIFICITY: Embryonic kidney, lung and placenta.
 -!- SIMILARITY: Contains 4 EGF-like domains.
 -!- SIMILARITY: Contains 2 VNFA domains.

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EMBL; AJ007581; CAA07569.1; -;
 EMBL; AL021578; CAC18104.1; -;
 EMBL; AL021578; CAC18105.1; -;
 HSSP; P00736; LAPQ.

Genew: HGNC:6910; MATN4.

MIM: 603897; C:extracellular; TAS.

GO; GO:0005576; Axon hydrolase; TAS.

InterPro; IPR000152; Axon hydrolase; TAS.

InterPro; IPR001881; EGF Ca.

InterPro; IPR006209; EGF-like.

InterPro; IPR002035; VNFA_A.

Pfam; PF00008; EGF; 4.

Pfam; PF00092; vwa; 2.

PRINTS; PR00453; VNFA000000.

SMART; SM00179; EGF CA; 1.

SMART; SM00327; VWA; 2.

PROSITE; PS00010; ASX HYDROXYL; 2.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS02334; VNFA; 2.

EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;

Alternative splicing.

SIGNAL 1 18 BY SIMILARITY.

CHAIN 19 619 MATRILIN-4.

DOMAIN 34 213 VNFA 1.

EGF-LIKE 1 (INCOMPLETE).

DOMAIN 215 253 EGF-LIKE 2.

DOMAIN 254 294 EGF-LIKE 3.

DOMAIN 295 335 EGF-LIKE 4.

DOMAIN 336 376 VNFA 2.

DOMAIN 384 559 VNFA 2.

DOMAIN 594 618 VNFA 2.

DOMAIN 219 230 BY SIMILARITY.

DISULFID 219 230 BY SIMILARITY.

DISULFID 226 239 BY SIMILARITY.

DISULFID 258 269 BY SIMILARITY.

DISULFID 265 278 BY SIMILARITY.

DISULFID 280 293 BY SIMILARITY.

DISULFID 299 310 BY SIMILARITY.

DISULFID 306 319 BY SIMILARITY.

DISULFID 321 334 BY SIMILARITY.

DISULFID 340 351 BY SIMILARITY.

DISULFID 347 360 BY SIMILARITY.

DISULFID 362 375 BY SIMILARITY.

CARBOHYD 69 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 251 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 303 N-LINKED (GLCNAC. . .) (POTENTIAL).

VARSPLIC 215 GNDQCAEGHGCHQHCQVNAWAMFHCTCNPYKLAADNKS

-> A (in isoform 2).

/FTID=VSP 001400.

R -> S (IN REF. 1).

M -> NL (IN REF. 1).

SEQUENCE 619 AA; 68190 MW; 2FICE3C9CC54B5D CRC64;

Query Match 12.3%; Score 431.5; DB 1; Length 619;

Best Local Similarity 23.7%; Pred. No. 8.8e-21;

Matches 131; Conservative 70; Mismatches 191; Indels 161; Gaps 12;

280 LEP-----VSLGDPNC---KIDSLFLIDGSTSIGKRRFRIQKQLADVAQAALDIPAGPLM 332
 14 LQWETQLQLTGPRTCTGFLDLVFDSSRSRVPPEFETMRQFLMGLLGLAVGPNATRV 73
 333 GVVOYGONPETHNLKTHNSRDLDKTALEKLTQRGGLSNVGRASIVFTVTKNFFSKANGNR- 391
 74 GVIQISSQVQVFPPLRAFSRRDMEALRDVPLAQGTWTGLAIQYAMNVAIVSVAEGARP 133
 392 --SGAPNVVVVMDGWPPTDKVEEASRLARESGINIFFITIEGA-----AENEKQ 438
 134 PEERVPRAVITDGRPODRAEVAQAARAGIBIYAVGVQADVGSLRAMASPPDLDEHV 193
 439 YVVE-----PNFANKAVCRTRNGFVSLH--VOSWPLGLHKTLOPLVVRVCDT-- 481
 194 FLVSEFDLIOBFGLOFQORLQCGKQCAEGHGHGCHQHCQVNAWAMFHCTCNPYKLAADNKS 253
 482 --DLRA-----CSKTCLNS-----ADIGPV----- 499
 254 SIDLCREGTGCHHCVNSPGSYFCHQVGVLPQDQSCRAIDYCSFGNHSCHQECVST 313
 500 ----- 499
 314 FGGPRCHCREGHDLPDGRSCQVRDLGNDVDRGCEFCQVSEGLSVRCLCPEGRLQADGK 373
 500 -----IDGSSSVGTCNFTVLOPVNTLKEPEISDTDTTIGAVQYTYEOR 544
 374 SCNRCREGHVDLVLDVLDGSKSVRPQNFELVRFVQNIQVDFDVSPGEGTVGLVQFSSVR 433
 545 LEFGDKYSSKPDILNAIKRYGWSGGTGTGAANFALBOLPKK---SKP---NKRKLM 598
 434 TEPPLGRYGTAAEVQAVLAVYMERGTWTGLALHMHVSESEAGQAPRALNVPVGL 493
 599 LITDGRSYDDVRIPAMAHLKGVITYAIGVAAQBELEVIATHPARDHSFPVDEPDNLH 658
 494 VPTDGRSQDDISVWAARAKEGIVMVYAVGVKGAZELREIASBPAELHVSVPADPGTMT 553
 659 QVVPRIIONICTE 671
 554 HLENLRGSIICPE 566
 RESULT 13
 MTN4 MOUSE STANDARD; PRT; 624 AA.
 AC O89029; O89030; O9QMS3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Matrilin-4 precursor (MAT-4).
 GN MATN4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND VARIANTS.
 RC STRAIN=C57BL/6J, and CD-1; TISSUE=Petal;
 RX MEDLINE=98442849; PubMed=9771906;
 RA Wagener R., Kobbe B., Paulson M.;
 RT "Matrilin-4, a new member of the matrilin family of extracellular
 matrix proteins.";
 RL FEBS Lett. 436:123-127 (1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM LONG).
 RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=1247732;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

GN MATN2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RX PubMed=1124542;
RA Muratoglu S., Krysan K., Balazs M., Sheng H., Zakany R., Modis L.,
RA Kiss I., Deak P.;
RT "Primary structure of human matrilin-2, chromosome location of the
RT MATN2 gene and conservation of an AT-AC intron in matrilin genes.";
RL Cytogenet. Cell Genet. 90:323-327(2000).
RN [2]
RP SEQUENCE OF 644-956 FROM N.A.
RX MEDLINE=97238663; PubMed=9083061;
RA Deak P., Piecha D., Bachrati C., Paulsson M., Kiss I.;
RT "Primary structure and expression of matrilin-2, the closest relative
RT of cartilage matrix protein within the von Willebrand factor type A-
RT like module superfamily.";
RL J. Biol. Chem. 272:9268-9274(1997).
RN [3]
RP SEQUENCE OF 244-956 FROM N.A.
RC TISSUE=Testis;
RA Duesterhoft A., Lauber J., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in matrix assembly (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O00339-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O00339-2; Sequence=VSP 001399;
CC -!- SIMILARITY: Contains 10 EGF-like domains.
CC -!- SIMILARITY: Contains 2 VWFA domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U69263; AAC51260.2; -;
DR EMBL; AL137638; CAB70853.1; ALT_INIT.
DR HSSP; P01132; LEGF.
DR Genew; HGNC:6908; MATN2.
DR MIM; 602108; -;
DR GO; GO:0005578; C:extracellular matrix; NAS.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR002035; VWFA.
DR Pfam; PF00008; EGF; 10.
DR Pfam; PF00092; vwa; 2.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00327; VWFA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 9.
DR PROSITE; PS01186; EGF_2; 9.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS00026; EGF_3; 4.
DR PROSITE; PS0234; VWFA; 2.
KW EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil;
KW Alternative splicing.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 956 MATRILIN-2.
FT DOMAIN 57 232 VWFA 1.
FT DOMAIN 238 278 EGF-LIKE 1.
FT DOMAIN 279 319 EGF-LIKE 2.
FT DOMAIN 320 360 EGF-LIKE 3.
FT DOMAIN 361 401 EGF-LIKE 4.

FT	DOMAIN	402	442	EGF-LIKE 5.
FT	DOMAIN	443	483	EGF-LIKE 6.
FT	DOMAIN	484	524	EGF-LIKE 7.
FT	DOMAIN	525	565	EGF-LIKE 8.
FT	DOMAIN	566	606	EGF-LIKE 9.
FT	DOMAIN	607	647	EGF-LIKE 10.
FT	DOMAIN	655	830	VWFA 2.
FT	DOMAIN	917	955	COILED COIL (POTENTIAL).
FT	DISULFID	242	253	BY SIMILARITY.
FT	DISULFID	249	262	BY SIMILARITY.
FT	DISULFID	264	277	BY SIMILARITY.
FT	DISULFID	283	294	BY SIMILARITY.
FT	DISULFID	290	303	BY SIMILARITY.
FT	DISULFID	305	318	BY SIMILARITY.
FT	DISULFID	324	335	BY SIMILARITY.
FT	DISULFID	331	344	BY SIMILARITY.
FT	DISULFID	346	359	BY SIMILARITY.
FT	DISULFID	365	376	BY SIMILARITY.
FT	DISULFID	372	385	BY SIMILARITY.
FT	DISULFID	387	400	BY SIMILARITY.
FT	DISULFID	406	417	BY SIMILARITY.
FT	DISULFID	413	426	BY SIMILARITY.
FT	DISULFID	428	441	BY SIMILARITY.
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FT	DISULFID	488	499	BY SIMILARITY.
FT	DISULFID	495	508	BY SIMILARITY.
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FT	DISULFID	529	540	BY SIMILARITY.
FT	DISULFID	536	549	BY SIMILARITY.
FT	DISULFID	551	564	BY SIMILARITY.
FT	DISULFID	570	581	BY SIMILARITY.
FT	DISULFID	577	590	BY SIMILARITY.
FT	DISULFID	592	605	BY SIMILARITY.
FT	DISULFID	611	622	BY SIMILARITY.
FT	DISULFID	618	631	BY SIMILARITY.
FT	DISULFID	633	646	BY SIMILARITY.
FT	CARBOHYD	221	221	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	890	890	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	861	879	Missing (in isoform Short).
FT	CONFLICT	356	356	/FTID=VSP_001399.
FT	CONFLICT	594	594	K -> E (IN REF. 3).
FT	CONFLICT	644	644	V -> E (IN REF. 3).
FT	CONFLICT	755	755	R -> G (IN REF. 2).
FT	CONFLICT	935	935	P -> L (IN REF. 3).
FT	CONFLICT	935	935	L -> F (IN REF. 2).
SQ	SEQUENCE	956 AA;	106840 MW;	826B7F347178FC80 CRC64;

Query Match 10.2%; Score 358.5; DB 1; Length 956;
Best Local Similarity 17.4%; Pred. No. 1e-15;
Matches 142; Conservative 80; Mismatches 189; Indels 405; Gaps 13;

QY	256	AFQKPVGADVSLGLVPKEELSTQSLSPVSLGDPNCKIDSLFDGTSIGKRFRIOKQL	315
DB	23	ARERSGRSISRGHARTHPTQALLES---SCENKRALVFIIDSSRSVYTHDYAKVRKP	79
QY	316	LADVAQALDIGPAGPLMGVVOYGDNPATPHNLKHTNSRDLTAKIKITQRCGLSNVGR	375
DB	80	IVDILQFLDIGDPVTRVGLLQYGSTVQNEFSLKTPRKSEVERAVRMHSLTGTWTGLA	139
QY	376	ISFVTKNFFSKANGN---RSGAPNVVVMVDGWPTDKVBEASRLARESGINIF-	425
DB	140	IQYALNIAFSRABGARPURENVPRVIMIVTDGRPDQSVAEVAAKARDTGILIFAGVGQV	199
QY	426	-FTIE--GAANEKQYVVEPNF-	445
DB	200	DFNTLKSGSBPHDHFVLFVANFSQITLTSVFQKCLCTAHMCSTLEHNCAHFINPGS	259
QY	446	-----ANKAVCR-	452
DB	260	YVCRCKQGIILNSDQTTCRIQDLCAEDHNCQLCVNVPFSGVQCYSYALABDGRCV	319

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QY 453 -----T 453
Db 320 AVDYCASENHGCEHCYNADSGSYLCOCHGEPALNPDKTKCTKIDYCASSNHGCHQECVNT 379
QY 454 NGFYSLHVQSWFGL-----HK--TLQP---473
Db 380 DDSYSCHCLGFTLNPDKTKRINYCALNKPGEHCVCNMBESYYCRCHRGYTLDPNGK 439
QY 474 -----473
Db 440 TCSRVDHCAQDHCBCQLCLNTEDSFVQCQSEGFLINEDLKTCRSDYVCLLSHGCHYSC 499
QY 474 -----473
Db 500 VNMDRSFACQCPGHLVRSQKCAKLDSCALGDHGCHEHSCVSSSEDSFVQCQPEGYILRE 559
QY 474 -----IV-----KRVCDTRDLACS 487
Db 560 DGKTCRRKDVCAIDHGCEHCIVNSDDSYTCECLVGFRLAEDGKRCKRKDYCKSTHGGCE 619
QY 488 KTCLSA-----DIGPVDGSSSVCTGNFRTVLQPV 519
Db 620 HICVNNNGSYICKSEGFVLAEDGRRCKCTEGPIDLVFDGSKSLGHEHFNFKQFVT 679
QY 520 NLTKPEPISDTRIGAVQYTYEQRLBFGFDKYSKEDILNAIKRVGVWSGTSTGAAIN 579
Db 680 GIIDSLTISPKAARVGLQYSTQVHTFTLNFNSAKDKKVAHMKYMGKSGMTGLAK 739
QY 580 FALBQLPK---SIPNKKKL---MILITDGRSYDDVRIPAMAHLKGVITYTAIGVAAWA 633
Db 740 HMPERSFTQSGARPPFTVRPAAIVFTDGRAODVSEWASAKAKANGITMYAVGVGKAIE 799
QY 634 EELEVIATHPARDHSFFVDEFDNLHQVPRILQNIC 669
Db 800 BELQEIASEPTNKLFLYAEFDFWDEISEKLRKGC 835

RESULT 15
MTN2_MOUSE STANDARD; PRT; 956 AA.
AC 008746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Matrilin-2 precursor.
GN MATN2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Limb;
RX MEDLINE=97238863; PubMed=9083061;
RA Deak F., Piecha D., Bachrati C., Paulsson M., Kiss I.;
RT "Primary structure and expression of matrilin-2, the closest relative
RT of cartilage matrix protein within the von Willebrand factor type A-
RT like module superfamily.";
RL J. Biol. Chem. 272:9268-9274 (1997).
CC CC -1- FUNCTION: Involved in matrix assembly (By similarity).
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC CC -1- TISSUE SPECIFICITY: Detected in a variety of organs, including
CC CC calvaria, uterus, heart and brain, as well as fibroblast and
CC CC osteoblast cell lines.
CC CC -1- SIMILARITY: Contains 10 EGF-like domains.
CC CC -1- SIMILARITY: Contains 2 VWFA domains.
-----
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CC -----
DR EMBL: U69262; AAC53163.1; -.
DR HSSP: P05099; 1A05.
DR MG: MGI:109613; Matn2.
DR GO: GO:0005578; C:extracellular matrix; IDA.
DR InterPro: IPR00152; Abx_hydroxyl_S.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; EGF.
DR InterPro: IPR002035; VWFA_A.
DR Pfam: PF00008; EGF; 10.
DR Pfam: PF00092; vwa; 2.
DR PRINTS: PR00453; VWFADOMAIN.
DR SMART: SM00181; EGF; 10.
DR SMART: SM00327; VWA; 2.
DR PROSITE: PS00010; ASX_HYDROXYL; 7.
DR PROSITE: PS01186; EGF_2; 9.
DR PROSITE: PS02034; VWFA; 2.
DR EGF-like domain; Signal; Glycoprotein; Repeat; Coiled coil.
KW SIGNAL 1 23
FT CHAIN 24 956
FT DOMAIN 57 232
FT DOMAIN 238 278
FT DOMAIN 279 319
FT DOMAIN 320 360
FT DOMAIN 361 401
FT DOMAIN 402 442
FT DOMAIN 443 483
FT DOMAIN 484 524
FT DOMAIN 525 565
FT DOMAIN 566 606
FT DOMAIN 607 647
FT DOMAIN 655 830
FT DOMAIN 917 955
FT DISULFID 242 253
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FT DISULFID 551 564
FT DISULFID 570 581
FT DISULFID 577 590
FT DISULFID 592 605
FT DISULFID 611 622
FT DISULFID 618 631
FT DISULFID 633 646
FT CARBOHYD 221 221
FT CARBOHYD 890 890
SQ SEQUENCE 956 AA; 106779 MW; 3B4C22770B6E6EE CRC64;
Query Match 9.6%; Score 337.5; DB 1; Length 956;
Best Local Similarity 17.4%; Pred. No. 2.4e-14;
Matches 140; Conservative 75; Mismatches 177; Indels 413; Gaps 14;
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SQ SEQUENCE 678 AA; 73930 MW; 9870E75A218C686C CRC64;
 Query Match 100.0%; Score 678; DB 4; Length 678;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRTVLTWASVIEMFLVLLVTGSHSNKETAACKIKRPFVTPQINCVDKAGKIIDPEFIV 60
 DB 1 MRTVLTWASVIEMFLVLLVTGSHSNKETAACKIKRPFVTPQINCVDKAGKIIDPEFIV 60

QY 61 KCPAGCQPKYHVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120
 DB 61 KCPAGCQPKYHVGTVDVYASVSSVCGAAVHSGVLDNSGGKILVRKVGAGSGYKGSYNG 120

QY 121 VQSLSLPRWRESFVLESKPKKGGVTPYSALTYSSKSPAAQAGETTKAYORPPPTGTTAQ 180
 DB 121 VQSLSLPRWRESFVLESKPKKGGVTPYSALTYSSKSPAAQAGETTKAYORPPPTGTTAQ 180

QY 181 PVTLMQLLAVTAVATPTTLRPPSPAASTTSIPRQSGVHRSQEMDLWSTATYTSSQNR 240
 DB 181 PVTLMQLLAVTAVATPTTLRPPSPAASTTSIPRQSGVHRSQEMDLWSTATYTSSQNR 240

QY 241 PRADPGIORQDPSGAAFOKPGADVSLGLVPKEELSTOSLEPVSIGDPNCKIDLSFLIDG 300
 DB 241 PRADPGIORQDPSGAAFOKPGADVSLGLVPKEELSTOSLEPVSIGDPNCKIDLSFLIDG 300

QY 301 STSICKRFRFQKQLLADVAQALDIPGAPLGMVQVQGNPDTHFNLTHTNSRDLKTAI 360
 DB 301 STSICKRFRFQKQLLADVAQALDIPGAPLGMVQVQGNPDTHFNLTHTNSRDLKTAI 360

QY 361 EKIITORGSLNVGRAISFVTKNFFSKANGRSGAPNVVVMVQDGPDKVEASRLARES 420
 DB 361 EKIITORGSLNVGRAISFVTKNFFSKANGRSGAPNVVVMVQDGPDKVEASRLARES 420

QY 421 GINIFPFIIEGAENEKQYVVEPNFANKAVCRITNGFTSLHVQSWFGLHKTLPVKVCD 480
 DB 421 GINIFPFIIEGAENEKQYVVEPNFANKAVCRITNGFTSLHVQSWFGLHKTLPVKVCD 480

QY 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNLTKFEISDITRIGAVQYT 540
 DB 481 TDLRACSKTCLNSADIGFVIDGSSVGTGNFRTVLQFVNLTKFEISDITRIGAVQYT 540

QY 541 YEORLEFGDKYSSKPDILNAIKRVYWSGTTSTGAAINFALQLFKSKPKNKKMLILI 600
 DB 541 YEORLEFGDKYSSKPDILNAIKRVYWSGTTSTGAAINFALQLFKSKPKNKKMLILI 600

QY 601 TDCRSYDDVRIIPAMAHLKGVITTAIGVAAQAQBELEVIATHPARDHSFFVDFDNLHGY 660
 DB 601 TDCRSYDDVRIIPAMAHLKGVITTAIGVAAQAQBELEVIATHPARDHSFFVDFDNLHGY 660

QY 661 VPRIIQNTCTEFNSQPRN 678
 DB 661 VPRIIQNTCTEFNSQPRN 678

RESULT 2

Q96DM8 ID Q96DM8 PRELIMINARY; PRT; 693 AA.
 AC Q96DM8
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ32210.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RT Tissue=Placenta;
 RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
 Hotta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
 Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,

RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Wagatsuna M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.,
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK056772; BAB71279.1; -;
 DR Genew; HGNC:12697; VIT.
 DR InterPro; IPR004043; LCCL dom.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF03815; LCCL; 1.
 DR Pfam; PF00092; Vwa; 2.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00603; LCCL; 1.
 DR SMART; SM00327; VWA; 2.
 DR PROSITE; PS0820; LCCL; 1.
 DR PROSITE; PS0234; WFA; 2.
 DR Hypothetical protein.
 SQ SEQUENCE 693 AA; 75575 MW; 2DE8B2421F2D496D CRC64;
 Query Match 60.6%; Score 411; DB 4; Length 693;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 268 GLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDGSTSIGKRRPRIQKQLLADVAQALDIP 327
 DB 268 GLVPKEELSTQSLPEVSLGDPNCKIDLSFLIDGSTSIGKRRPRIQKQLLADVAQALDIP 342

QY 328 AGPLMGVQVQGNPDTHFNLTHTNSRDLKTAIEKIQRGGLSNVGRASIFVTKNPFSA 387
 DB 343 AGPLMGVQVQGNPDTHFNLTHTNSRDLKTAIEKIQRGGLSNVGRASIFVTKNPFSA 402

QY 388 NGRSGAPNVVVMVQDGPDKVEASRLARESINIFITIEGAENEKQYVVEPNFAN 447
 DB 403 NGRSGAPNVVVMVQDGPDKVEASRLARESINIFITIEGAENEKQYVVEPNFAN 462

QY 448 KAVCRITNGFTSLHVQSWFGLHKTLPVKVCDTDLRACSKTCLNSADIGFVIDGSSV 507
 DB 463 KAVCRITNGFTSLHVQSWFGLHKTLPVKVCDTDLRACSKTCLNSADIGFVIDGSSV 522

QY 508 TGNFRTVLQFVNLTKFEISDITRIGAVQYTYEORLEFGDKYSSKPDILNAIKRVGY 567
 DB 523 TGNFRTVLQFVNLTKFEISDITRIGAVQYTYEORLEFGDKYSSKPDILNAIKRVGY 582

QY 568 WSGTSTGAAINFALQLFKSKPKNKKMLITDGRSYDDVRIIPAMAHLKGVITTAIG 627
 DB 583 WSGTSTGAAINFALQLFKSKPKNKKMLITDGRSYDDVRIIPAMAHLKGVITTAIG 642

QY 628 VAAQAQBELEVIATHPARDHSFFVDFDNLHGYVPRIIQNTCTEFNSQPRN 678
 DB 643 VAAQAQBELEVIATHPARDHSFFVDFDNLHGYVPRIIQNTCTEFNSQPRN 693

RESULT 3

Q96DT1 ID Q96DT1 PRELIMINARY; PRT; 656 AA.
 AC Q96DT1
 DT 01-DEC-2001 (TremBLrel. 19, Created)
 DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
 DE Vitrin.
 GN VIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Skeletal muscle, and Fetal heart;
 RA Ren Z.-X., Liu J.G., Mayne R.;
 RT "Human vitrin complete cDNA sequence.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.